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June 19, 2004, 01:57:22; Search time 1844 Seconds (without alignments) 7827.131 Million cell updates/sec
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1 cagtotgccccgactcagcc.....cccggttgaccgtcctaggt 333
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB seq length: 333
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1 AB064024 LOCUS DEFINITION	AB064024 Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, parrial cds. clone:1153.
ACCESSION VERSION	AB064024 AB064024.1 GI:21669254
KEYWORDS SOURCE	Homo sapiens (human)
ORGANISM	Homo saplens Bukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
REPERENCE AUTHORS	1 Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,

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SOURCE
ORGANISM
                                                                             REFERENCE
AUTHORS
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MEDLINE
PUBMED
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TITLE
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<1. .>3335
/gene="IGL"
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GGTKLTVLG"
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Miura, K. and Kurosawa, Y. Construction of antibody libraries: isolation of therapeutic human antibodies and application to functional
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/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
1. .333
                                                                                                  Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toycake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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/clone="L153"
                                              genomics
Unpublished
2 (bases 1 to 333)
Kurosawa, Y.
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HSA199863
HOMO sapiens partial mRNA for thyroid peroxidase-specific immunoglobulin lambda chain variable region (IGLV gene), clone B10. AJ399863.1 GI:9968427
IGLV gene; immunoglobulin lambda chain; immunoglobulin light chain,

ACCESSION VERSION KEYWORDS

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Chapal,N., Chardes,T., Bresson,D., Pugniere,M., Mani,J.C., Pau,B., Bouanani,M. and Peraldi-Roux,S. Thyroid peroxidase autoantibodies obtained from random single chain FV libraries contain the same heavy/light chain combinations as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /country="France"
/note="Anti-thyroid peroxidase scPv fragment isolated from
a phage display combinatorial library"
1. .333
/gene="IGLV"
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Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chapal,N.
Direct Submission
Submitted (05-JAN-2000) Chapal N., Faculte de Pharmacie, CNRS Submitted (05-JAN-2000) Chapal N., Faculte de Pharmacie, CNRS UMR9921, 15 avenue Charles Flahault, Montpellier 34060, FRANCE Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region"
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87.0%; Score 289.8; DB 9; Length 333;
Best Local Similarity 91.9%; Pred. No. 5.9e-74;
Matches 306; Conservative 0; Mismatches 27; Indels 0
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//rearranged
                                                                                                                                                                                                                                                                                                                                                                                                              occur in vivo
Endocrinology 142 (11), 4740-4750 (2001)
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2 (bases 1 to 333)
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Direct Submission Submitted (14-MAY-1998) Fais F., Clinical Immunology, Istituto Nazionale per la Ricerca sul Cancro, L.go R. Benzi 10, 16132, ITALY Location/Qualifiers HSA006162 331 bp mRNA linear PRI 20-JUL-1999 Homo sapiens mRNA for variable region of Ig light chain, rearrangement of BC2 cell line). 120 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240 241 CAGGCTGAGGACGAGGCTGATATTACTGCAGCTCATATACAAGCAGCAGCACTTATGT 300 61 TCCTGCACTGGAACCAGCAGTGACATTGGTGGTTATAATTATGTCTCCTGGTACCAACAA 120 240 240 9 AJ006162 AJ006162. AJ006162. AJ006162. Home sapiens (human) Home sapiens (human) Home sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1] ,330 /gene="V12a2 gene" /product="variable region of immunoglobulin light chain" 9 Fais, P., Gaidano, G., Capello, D., Gloghini, A., Ghiotto, F., Roncella, S., Carbone, A., Chiorazzi, N. and Ferrarini, M. Immunoglobulin V region gene use and structure suggest antigen selection in AIDS-related primary effusion lymphomas 61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC CAGGCTGAGGACGAGGCTGATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 1 caercrececeacreaccrecererererereserereseaceacreseresere Gaps /note="derived from AIDS-related primary effusion lymphoma" ; Length 331; /mol_type="mRNA"
/db_xref="taxon.9606"
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0y 241 CA Db 241 CA Oy 301 TT Db 701 TT	RESULT 6 AF194604 LOCUS LOCUS DEFINITION HOMO ACCESSION AF19 VERSION AF19 VERSION AF19 KEYWORDS SOURCE HOMO ORGANISM HOMO ORGANISM HOMO AUTHORS IGNA AUTHORS IGNA MEDLINE 2007 PUBMED 1061 AUTHORS IGNA TITLE JOURNAL J. MAIN COURNAL J. MAIN TITLE IGNA MEDLINE 2007 PUBMED 1061 AUTHORS IGNA TITLE JOURNAL SUDM PUBMED 1061 AUTHORS IGNA MINE TITLE JOURNAL SUDM FEATURES SOURCE	ORIGIN Query Match Best Local Sim Matches 303; QY
Qy 241 CAGGCTGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	RESULT 5 AF194592 LOCUS LOCUS LOCUS LOCUS LOCUS ACCESSION PROPER CLONE 1407 immunoglobulin lambda light chain variable region manA, partial cds. AF194592. LOCUS AF194592. AF194592. AF194592. GRANISM RESION AF194592. AF194592. GRANISM REALTYCE (Mono sapiens (human) REMARTYCE (Homo sapiens (human) RAMARTYCE (Homo sapiens (human) RAMARTYCE (Homo sapiens (human) RAMARTYCE (Homo sapiens (human) RAMARTYCE (Homo sapiens (human) AUTHORS (Homo sapiens (human) REPERENCE (Homo sapiens (human) AUTHORS (Human) AUTHOR) MENDING (Homo sapiens (human) JOURNAL (Homo sapiens (human) AUTHORS (Human) AUT	Cuery Match Guery Match Best Local Similarity 91.8%; Pred. No. 4.5e-73; Matches 303; Conservative 0; Mismatches 27; Indels 0; Gaps 0; Qy Cagronococconstruction Cagronocorrococrococcoccoccoccoccoccoccoccocco

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194604 330 bp mRNA linear PRI 10-JAN-2000 no sepiens clone 919 immunoglobulin lambda light chain variable langen mRNA, partial cds.
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omitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Hills
ad, Cambridge CB2 20H, UK
Location/Qualifiers
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380kb region of human Ig lambda locus DNA"
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larity 91.8%; Pred. No. 4.5e-73;
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uncoglobulin Vlambda repertoire
Mol. Biol. 294 (2), 457-465 (1999)
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qq	181 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGTC 240		
à	241 CAGGCTGAGGAGGCTGATTATTACTGTTGATACAACCAGTAGCACTTTGTTA 300	Ši t	
qq	241 CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCACTCTGGTA 300	<u>8</u> 8	121 CACC
Qy Db	301 TTCGGAAGAGGACCCGGTTGACCGTCTA 330	ž 8	
RESULT 7		& 8 8	241 CAGGC 241 CAGGC
AB063978 LOCUS DEFINITION ACCESSION	AB063978 333 bp mRNA linear PRI 02-JUL-2002 Fomo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, partial cds, clone:L107. AB063978	& &	301 TTCGC 301 TTCGC
VEKSION KEYWORDS SOURCE ORGANISM		RESULT 8 HSIGLOUR LOCUS DEFINITION	
REFERENCE AUTHORS		ACCESSION VERSION KEYWORDS SOURCE	
TITLE	Miura, K. and Kurosawa, Y. Construction of antibody libraries: isolation of therapeutic human antibodies and application to functional	ORGANISM	Homo se Eukaryo Mammali
JOURNAL REFERENCE		REFERENCE AUTHORS	1 Ravira Martin,
AUTHORS	Kurosawa,Y. Direct Submission	TITLE	Genetic
JOURNAL		JOURNAL	Eur. J 9814375
the state of the s	<pre>Kucsukake-cno, 10yoake 4/U-1192, Japan (E-mail:kuroswa@fujita-hu.ac.jp, Tel:81-562-93-9387)</pre>	REFERENCE	2 (bas
FEATURES	Trans visit of the out at joinmunity/. URL:http://www.fulita.nc.jp/immunity/. Location/Qualifiers	TITLE	Direct
source		-	Totten
	<pre>/wol_type="mRNA" /db_xref="taxon:9606" /clone="Li07" /clone="Lib7" /note="mixture of tissues:tonsils, umbilical cords,</pre>	PEATURES SOURCE	σ)
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QQ	1 CAGICTGCCCTGACTCAGCCTCAGTGTCCCCGGGTCTCCTGGACAGTCACCATC 60	misc	misc_feature
ò	61 TCCTGGACTGGAACCAGGGATGACGTTGGTGATAACTATGTCTCCTGGTACCAACAC 120	ORIGIN	
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| noncelevariable region
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| /db_xref="REWTREMBL:CAA65054" |
| /db_xref="REWTREMBL
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in,A.C., Ehrenstein,M.R., Latchman,D.S. and Isenberg,D.A.
ic, structural and functional properties of an IgG DNA-binding
lonal antibody from a lupus patient with nephritis
J. Immunol. 28 (1), 339-350 (1998)
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IM.A.A.

tt Submission

tted (16-FEB-1996) M.A.A. Rahman, Bloomsbury Rheumatology
University College London, Arthur Stanley House, 40-50

inham Street, London WIP 9PG, UK

Location/Qualifiers
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AF194586 330 bp mRNA linear PRI 10-JAN-2000 Homo sapiens clone 1233 immunoglobulin lambda light chain variable region mRNA, partial cds.
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Submitted (13.0cr-1999) Laboratory of Molecular Biology, MRC, Hills
Road, Cambridge CB2 20H, UK
Location/Qualifiers
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181 CCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 330)
Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and
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Dominance of intrinsic genetic factors in shaping the human immunoglobulin Vlambda repertoire
20. Mol. Biol. 294 (2), 457-465 (1999)
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   Length 330;
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 Query Match 85.6%; Score 285.2; DB 9; Best Local Similarity 91.5%; Pred. No. 1.3e-72; Matches 302; Conservative 0; Mismatches 28;
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Direct Submission
Submitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Hills Road, Cambridge CB2 20H, UK
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Homo sapiens clone 1034 immunoglobulin lambda light chain variable
REGion mRNA, partial cds.
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gnatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and
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 Pred. No. 5.1e-73;
0; Mismatches 29; Indels
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Best Local Similarity 91.3%;
Matches 304; Conservative
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Homo sapiens clone 1343 immunoglobulin lambda light chain variable region mRNA, partial cds.
AF194589
AF194589.1 GI:6643176
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121 CACCCAGGCAAAGCCCCCAAACTCATGAGAGTCAGTAATCGGCCCTCAGGGGTT 180
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1 (bases 1 to 330)
Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Winter,G.
Dominance of intrinsic genetic factors in shaping the human farmonoglobulin Vlambda repertoire

J. Mol. Biol. 294 (2), 457-465 (1999)
                                                                                                                                                                                                              61 TCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTATGTCTCCTGGTACAACAG
                                                                                                                                   1 CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCCTGGACAGTCGATCCATC
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                                                                          Gaps
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Direct Submission
Submitted (13-OCT-1999) Laboratory of Molecular Biology, MRC, Road, Cambridge CB2 20H, UK
Road, Cambridge CB2 20H, UK
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/product="immunoglobulin lambda light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 330)
Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M.
                                                                          ö
                                     Length 330;
                                   Query Match 85.6%; Score 285.2; DB 9; Length Best Local Similarity 91.5%; Pred. No. 1.3e-72; Matches 302; Conservative 0; Mismatches 28; Indels
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/clone="1343"
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Homo sapiens
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AF194587.1 GI:6643172
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Direct Submission
Direct Submission
Submitted (13-0CT-1999) Laboratory of Molecular Biology, MRC, Hills
Road, Cambridge CB2 20H, UK
Road, Cambridge CB2 20H, UK
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121 CACCCAGGCAAAGCCCCCAAACTCATGATTATGAGGTCAGTAATCGGCCCTCAGGGGTT 180
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                                                                                      Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and
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380kb region of human Ig lambda locus DNA"
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region"
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Ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and
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Dominance of intrinsic genetic factors in shaping the human immunoglobulin Vlambda repertoire
J. Mol. Biol. 294 (2), 457-465 (1999)
20079509
                                                       ö
              Query Match 85.6%; Score 285.2; DB 9; Length 330; Best Local Similarity 91.5%; Pred. No. 1.3e-72; Matches 302; Conservative 0; Mismatches 28; Indels 0.
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/organiam="Homo sapiens"
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APKIMIYEVSNRPSGVSNRFSGSKSGNTASLJISGLQAEDEADYYCSSYTSSSTLVFG GGTKLIVL

330 bp mRNA linear PRI 10-JAN-2000 Homo sapiens clone 943 immunoglobulin lambda light chain variable AF194608 AF194608.1 GI:6643214 Winter, G.
Direct Submission
Submitted (13-0CT-1999) Laboratory of Molecular Biology, MRC, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers ö 181 TCTGATCGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCCCGGACCATCTCTGGGCTC 240
181 TCTAATCGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTGGGCTC 240 121 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGAGGTCAGTAATCGGCCCTCAGGGGGTT 180 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300 241 CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCAGCTCTGGTG 300 121 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180 9 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 330)

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1 (parevich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Winter,G. 1 casicrescereacrescerecerecerereserecereacastes are 1 CAGTOTACCCCGACTCAGCCTCCCTCTGTGTCTCGGGTCTCCTGGACAGTCGGTCACCATC Gaps 2 (bases 1 to 330)
ignatovich,O., Tomlinson,I.M., Popov,A.V., Bruggemann,M. and Dominance of intrinsic genetic factors in shaping the human immunoglobulin Vlambda repertoire J. Mol. Biol. 294 (2), 457-465 (1999) 20079509 ö Length 330; Query Match 85.6%; Score 285.2; DB 9; Length Best Local Similarity 91.5%; Pred. No. 1.3e-72; Matches 302; Conservative 0; Mismatches 28; Indels

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Homo sapiens clone BY-12LC IgM light chain variable region mRNA,
U76676
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PKLMYIPEVSNRPSGVSNRFSGSKSGNTASLTISGLQARDEADYYCSSYTSSSTGVFG
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181 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACAGGCCTCCCTGACCATCTCTGGGCTC 240
                                                                                                                                                                                 121 CACCCAGGCAAAGCCCCCAAACTCATGATTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
121 CACCCAGGCAAAGCCCCCAAACTCATGATTATGAGGTCAGTAATCGGCCCTCAGGGGTT 180
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241 CAGGCTGAGGAGGAGGGCTGATTATTACTGCAGCACAGCAGCACTGGGGTG 300
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 333)
Aguilera,I., Melero,J., Nunez-Roldan,A. and Sanchez,B.
Molecular structure of eight human autoreactive monoclonal
                                                                                                                             9
                                                                                                                                            1 CAGTCTGCCCTGACTCAGCCTCCGTGTCTGGGTCTCCTGGACAGTCGACCATC 60
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Aguilera 1.
Aguilera 1.
Subrict (30:007-1996) Hospital U. Virgen del Rocio, Immunology,
Manuel Siurot s/n, Seville, Spain, 41013
                                                                                                                           1 CAGTUTGCCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACTCGGGTCGCCCATC
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                                                                   Query Match
Best Local Similarity 91.5%; Pred. No. 1.3e-72;
Matches 302; Conservative 0; Mismatches 28; Indels 0
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181 CCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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                                                  Gaps
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                    Query Match 85.6%; Score 285; DB 9; Length 333; Best Local Similarity 91.0%; Pred. No. 1.5e-72; Matches 303; Conservative 0; Mismatches 303; Indels
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June 19, 2004, 01:55:31; Search time 276 Seconds (without alignments) 5125.543 Million cell updates/sec
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1 cagtctgccccgactcagcc......cccggttgaccgtcctaggt 333
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                US-09-019-441A-1_COPY_58_390
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Maximum Match 100%
Listing first 45 summaries
                                                                        - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					SOMESTES		
Result No.	Score	Query Match	Query Match Length DB	98	OI.	Description	
	280.8	84.3	333	4	AAH42407	Aah42407 Nucleotid	
N	280.8	84.3		4	AAH42401	Aah42401 Nucleotid	
m	275.8	82.8	330	ø	ABX00191	Abx00191 Mouse DNA	
4	275.8	82.8	330	v	ABK71397	Abk71397 Thrombopo	
ເກ	275.4	82.7	333	(V)	AAT10327	Aat10327 Human ant	
9	275.4	82.7	333	N	AAZ31655	Aaz31655 Coding se	
7	273.8	82.2	333	N	AAZ31654	Aaz31654 Coding se	
œ	270.8	81.3		ব	AAS03477	Aas03477 DNA encod	
σι	269.2	80.8	330	4	AAS03520	Aas03520 DNA encod	
10	265.8	79.8		N	AAQ55659	Aag55659 Monoclona	
11	262.8	78.9	330	œ	ACC85452	Acc85452 Human gly	
12	248.4	74.6		4	AAF58706	Aaf58706 Huntingti	
13	243.6	73.2		9	AAD46293	Aad46293 Human KDR	
4.1	243.6	73.2		7	ABT23328	Abt23328 VEGF bind	
15	243.6	73.2		Q	ADD24421	Add24421 Human lig	
91	243.6	73.2		φ	ADD80798	Add80798 Human clo	
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19	242	72.7	330	σ	ADD24431	Add24431 Human lig	
20	242	72.7	330	άJ	ADD80808	Add80808 Human KDR	
21	239.6	72.0		ហ	AAH68682	Aah68682 Human ant	
22	239.6	72.0	324	œ	ACD45346	Acd45346 Anti-Rh(D	
23	239.2	71.8	300	m	AAA52443	Aaa52443 Wild-type	

	Aai51083 Probe #19	Probe	Aak45127 Human bon	Aak19166 Human bra	Abs44798 Human liv	Abs19377 Human gen	Aaa52446 High affi	Aaa56720 HuIglambd		Aas03506 DNA encod	Aaa56719 Human Ig	Aaa56724 HuIglambd	Aaa56723 Human Ig	Aah68683 Human ant	Acd45347 Anti-Rh(D	Ada89167 Human ant	Aas03527 DNA encod	Aai68771 Human aut	Aas03458 DNA encod	Aas03485 DNA encod	Aas03529 DNA encod	
ABA70898	AA151083	ABA37341	AAK45127	AAK19166	ABS44798	ABS19377	AAA52446	AAA56720	PAA52444	AAS03506	AAA56719	AAA56724	AAA56723	AAH68683	ACD45347	ADA89167	AAS03527	AA168771	AAS03458	AAS03485	AAS03529	
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71	71	71	7.1	71	71	71	7.0	69	68	68	99	63	9	62	62	9	9	9	EQ.	5	53	
237	237	23.7	23.7	237	237	237	234.4	230	228	227.4	220.8	212.4	211.2	208.8	208.8	202	201.8	201.4	198.6	198.4	197	
24	25	26	27	28	56	30	31	75	33	34	35	36	7	88	ι (N	40	41	42	4	44	45	

ALIGNMENTS

Antibody, light chain; VL, amyloid protein, blood brain barrier; endothelial cell, brain cell antigen; inflammation; adhesion molecule; transferrin receptor; neurological disease, Alzheimer's disease; prion disease; Ansheren antigens prion disease; Ansheren injury; se. Nucleotide sequence of variable light chain fragment of clone G102 ВР. AAH42407 standard; DNA; 333 (first entry) 01-OCT-2001 AAH42407; RESULT 1
AAH42407
XX AAH4
XX AAH4
XX AAH4
XX AAH1
XX A

Homo sapiens

WO200144300-A2.

21-JUN-2001.

27-NOV-2000; 2000WO-GB004501.

99US-0170599P. 13-DEC-1999; (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Webster C, Osbourn J, Ward G, Miller K,

WPI; 2001-398131/42. P-PSDB; AAG62963.

Mixture or panel of antibodies for selecting specific binding members that cross the blood brain barrier, for use in delivering different molecules and treating neurological diseases.

Disclosure; Page 106; 109pp; English.

The present sequence encodes an antibody variable light chain (VL) fragment. The fragment is used to produce a mixture or panel of 5 different specific binding members, each comprising an antibody VH and/or VL variable domain and capable, when displayed on the surface of filamentous bacteriophage particles or in the case of a specific binding member comprising the DS VH and/or VL variable domain when bound to human serum amyloid protein, to pass through a mammalian blood brain barrier (BBB). The panel is useful for the selection of specific binding members

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with a desired property such as ability to cross BBB, ability to bind endochelial cells or other brain cell antigen, ability to bind areas of inflammation in the brain or BBB breakdown or ability to bind intracellular adhesion molecules and to bind transferrin receptor. The antibodies are useful in diagnosis, prophylaxis and treatment of human or animal body, including neurological diseases, such as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy and traumatic brain injury and any diseases involving inflammation occurring within the brain or central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTGCACTGGAACCAGCGATQACGTTGGTGGTATAACTATGTCTCCTGGTACCAACAC 120
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84.3%; Score 280.8; DB 4; Length
Best Local Similarity 90.4%; Pred. No. 4.8e-78;
Matches 300; Conservative 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 333 BP; 72 A; 99 C; 86 G; 76 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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Antibody; light chain, VL, amyloid protein; blood brain barrier; endothelial cell; brain cell antigen; inflammation; adhesion molecule; transferrin receptor; neurological disease; Alzheiner's disease; prion disease; Alsheiner's disease; prion disease; Alsheiner's disease;
                                                                             Nucleotide sequence of variable light chain fragment of clone G93
                                                                                                                                                                                                                                                                     (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
                                                                                                                                                                                                                                                                                           Ward G,
              ВÞ
                                                                                                                                                                                                                         27-NOV-2000; 2000WO-GB004501
             AAH42401 standard; DNA; 333
                                                        (first entry)
                                                                                                                                                                                                                                                                                           Webster C, Osbourn J,
                                                                                                                                                                               WO200144300-A2.
                                                                                                                                                           Homo sapiens
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                                                        01-OCT-2001
                                  AAH42401;
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WO200233073-A1

WPI; 2001-398131/42. P-PSDB; AAG62957.

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The present sequence encodes an antibody variable light chain (VL)

fragment. The fragment is used to produce a mixture or panel of 5

different specific binding members, each comprising an antibody VH and/or

CV Variable domain and capable, when displayed on the surface of

filamentous bacteriophage particles or in the case of a specific binding

comender comprising the BS VH and/or VL variable domain when bound to human

compression in the SVH and/or VL variable domain when bound to human

compression anyloid protein, to pass through a mammalian blood brain barrier

compression is useful for the selection of specific binding members

compression in the brain or BBB breakdown or ability to bind

condition in the brain or BBB breakdown or ability to bind

contracellular adhesion molecules and to bind transferrin receptor. The

antibodies are useful in diagnosis, prophylaxis and treatment of human or

animal body, including neurological diseases, such as Alzheimer's

disease, prion disease, AIDS-related dementia, epilepsy and traumatic

brain or central nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FCCTGCACTGGAACCAGCAGTGACGTTGATAAACTATGTCTCCTGGTACCAACAA 120
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Mixture or panel of antibodies for selecting specific binding members that cross the blood brain barrier, for use in delivering different molecules and treating neurological diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CACCCCAGGCAAAGCCCCCCAAAGTCATGATTATGAGGGCAGTAAGCGGCCCTCAGGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 333 BP; 71 A; 99 C; 87 G; 76 T; 0 U; 0 Other;
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84.3%; Score 280.8; DB 4;
Best Local Similarity 90.4%; Pred. No. 4.8e-78;
Matches 300; Conservative 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCGCCGAGGGACCAAGCTGACCGTCCTAGG 332
                                                                                   Disclosure; Page 103; 109pp; English
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BP

DNA; 330

standard,

ABK71397

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The invention relates to a new modified single chain FV antibody

containing at least two Heavy chain variable domains and at least two

Light chain variable domains from the same or different monochonal

antibodies and which is an agonist for crosslinking a molecule at the

cell surface or within the cell and thereby transducing a signal into the

cell surface or within the cell and thereby transducing a signal into the

cell surface or within the cell and thereby transducing a signal into the

cell surface or within the cell and thereby transducing a signal into the

nicroorganisms transformed by and expressing the preparation of

the antibodies by culture of the transformed cells, drug compositions

containing the antibodies and an assay method for the agonist activity of

the antibodies by contacting the antibodies with cells expressing the

cheaten and prevention of cancer, inflammatory disease, hormonal

disorders including diabetes, autoimmune disease, leukaemia,

dysendocrinism and blood disorders. The present sequence is a DNA

sequence encoding an antibody of the invention or a fragment thereof
                                                                                                                                                                                                                                                                                                                                                                        Modified single chain multimeric Fv antibody acting as a signal transduction agonist for treatment of inflammatory hormonal and blood disorders and cancer.
                                                                                                                                                                                                                                                                          Tsunoda
                                                                                                                                                                                                                                                                          Yabuta N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 330 BP; 73 A; 100 C; 83 G; 74 T; 0 U; 0 Other;
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                                                                                                                     20-OCT-2000; 2000JP-00321822.
12-MAR-2001; 2001WO-JP001912.
17-APR-2001; 2001WO-JP003288.
12-SEP-2001; 2001JP-00277314.
                                                            22-OCT-2001; 2001WO-JP009260.
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                                                                                                                                                                                                                              (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                      Tsuchiya
                                                                                                                                                                                                                                                                                                            WPI; 2002-682599/73.
P-PSDB; ABG97830.
                                                                                                                                                                                                                                                                      Fukushima N,
                                                                                                    20-OCT-2000;
                    25-APR-2002
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4 TCTGCCCCGACTCAGCCTCCCTCTGGGTCTCCTGGACAGTCGGTCACTCC ö Query Match 82.8%; Score 275.8; DB 6; Length 330; Best Local Similarity 90.2%; Pred. No. 1.8e-76; Matches 295; Conservative 0; Mismatches 32; Indel9 0.

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                                                                                                                                  GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTTC 303
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               63
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                                                                                                    244 GCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAACCAGAAGCACTCGGGTGTTC
                       4 TATGEGEGACTCAGCCACCTCGGTGTCAGGGTCTCCTGGACAGTCGATCACCATCTCC
                                                                         CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGGCCTCAGGGGTCTCT
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RESULT 4

243 243 303 303

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The invention describes a modified antibody comprising at least 2 heavy cathair variable domains and 2 or more light chain variable domains of an antibody, and exhibits thrombopietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia for platelet reduction-associated alseases, can act as a TPO signal transduction agonist by transducing a signal into ells by crosslinking a TPO receptor to exert TPO agonism. This sequence represents thrombopoletin (TPO) agonist antibody associated polymucleotide used in the creation of the modified antibody described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTGCGCTAAGCGGGCCTCAGGGGTCTCT 183
124 CCAGGCAAAGCCCCCAAACTCATGATTTATGAGGCAGTAAAAGGCCCTCAGGGGTTTCT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies folood diseases, thrombopenia following cancer chemotherapy or leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACACAGTCGGTCACCATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TATGTGCTGACTCAGCCACCTCGGTGTCAGGGTCTCCTGGACAGTCGATCACCATCTCC
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                                                                                                        Thrombopoietin (TPO) agonist antibody associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                      Modified antibody; thrombopoietin; TPO; agonist; TPO receptor; platelet reduction-associated blood disease; thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsunoda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 8; Page 198-199; 213pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                      20-OCT-2000; 2000JP-00321821.
17-APR-2001; 2001WO-JP003288.
12-SEP-2001; 2001JP-00277314.
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                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              (CHUS ) CHUGAI SEIYAKU KK.
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Best Local Similarity 90.23
Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Esuchiya M, Obtomo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4PI; 2002-383513/41.
                                                                                                                                                                                                                                                WO200233072-A1.
                                                                      30-JUL-2002
                                                                                                                                                                                                                                                                                    25-APR-2002
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This sequence encodes a VL domain complementarity determining region (CDR) from an antibody specific for estradiol. The invention relates to specific binding members (Sbp) comprising a polypeptide that comprises an antibody antigen binding domain (AABD) which has a dissociation constant of less than 1.0x10^8M for estradiol, and a dissociation constant less than 1.0x10^8M for estradiol, and a dissociation constant test cost of 10 dipher for the steroid hormones selected from estriol, testosterone, dihydrotestosterone, progesterone, estriol 3-suphate and estriol 4 domain. The Sbps can be used in an immunosasy for action mitthody WH domain. The Sbps can be used in an immunosasy for used for monitoring estradiol levels, e.g. during the menstrual cycle, in hormone replacement therapy and for diagnosing oestrogen secreting thurours. The Sbps can provide for discrimination between estradiol and other related steroids
181 TCTACTCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Estradiol; complementarity determining region; CDR; estriol-3-sulphate; antibody antigen binding domain; steroid hormone; estriol; testosterone; eihydrotestosterone; progesterone; estriol 3-beta-di-glucuronide; menstrual cycle; hormone replacement therapy; oestrogen secreting tumour; diagnosis; VL domain; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGICTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATC 60
                                                                                                          241 CAGGCTGAGGACGAGGCTGAATATTACTGCAGCTCACATGCAATCACCAGCACTCTCATA
                                                                               241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTGTATACAACCAGTAGCACTTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New specific binding partners for estradiol, used for monitoring estradiol levels during the menstrual cycle, in hormone replacement therapy and for diagnosing estrogen secreting tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 82.7%; Score 275.4; DB 2; Length 333; Best Local Similarity 89.2%; Pred. No. 2.4e-76; Matches 297; Conservative 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VL domain CDR of anti-estradiol antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 333 BP; 68 A; 101 C; 84 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pritchard K, Williams AJ;
                                                                                                                                                                              301 TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                               301 TrcGGGGGAGGGACCAAGCTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 27-28; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-00958201.
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                                                                                                                                                                                                                                                                                                                                                                AAZ31655 standard; DNA; 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pope AR,
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P-PSDB; AAY43257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coding sequence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ31655;
                                                                                                                                                                                                                                                                                                               RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes the light chain variable region of a human antibody which specifically recognises a lipopolysaccharide (LPS) antigen from Pseudomonas a seruginosa. The coding sequence can be used for preparing cell lines which produce monoclonal antibodies against the LPS. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTGGCTAAGCGGGCCTCAGGGGTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "VL_chain"
/note= "coding region does not include start or stop
codons"
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immunoglobulin; IgM; lambda light chain; variable region;
lipopolysaccharide; LPS; antigen; Pseudomonas aeruginosa; type B;
monoclonal antibody; 88.
                                                                                                                                                                                                                                                                                                                                                                                        Human anti-Pseudomonas aeruginosa type B antibody VL region cDNA
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89.2%; Pred. No. 2.4e-76;
live 0; Mismatches 36; Indels 0.
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                              GGAAGAGGACCCGGTTGACCGTCCTA
                                                                                                                                                                                                          AAT10327 standard; cDNA to mRNA; 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens; (cell line MP-5097).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MITK ) MITSUI TOATSU CHEM INC.
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(first entry)
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Best Local Similarity 89.2
Matches 297; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-072335/08.
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                                                                                                                                                                                                                                                                                                            16-OCT-2003
18-JUL-1996
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used for monitoring estradiol levels, e.g. during the menstrual cycle, hormone replacement therapy and for diagnosing oestrogen secreting tumours. The sbps can provide for discrimination between estradiol and other related steroids

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Sequence 333 BP; 68 A; 100 C; 84 G; 81 T; 0 U; 0 Other;

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9 9 240 240

120

180 61 TCCTGCACTGGAACCAGCGATGACGFTGGTGATAACTATGTCTCCTGGTACCAACAC 120 241 CAGGTTGAGGAGGCTGATTATTACTGCAGCTCACTTACACGCAGAGTCACTGTGATC 300 180 CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300 Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases. AAS03401-AAS03535 represent anti-adipocyte monoclonal antibody heavy and 121 CACCCCAGGCAAAGCCCCCAAACTCATGAGGTTTTTTGAGGTCAGTAATCGGCCCTCAGGGGTT 181 TCTGATCGCTTCTGGCTCCAAGFCTGGCAACAGGCCTCCCTGACCATCTCTGGGCTC
181 CCTAATCGCTTCTCAGGCTCCAAGTCTGGGAACAGGCCTCCCTGACCATCTCTGGGCTC CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 1 cagrerdeceeegacrecatecreerererererecerecacaeresereaceare Gaps 64. ö 2; Length 333; DNA encoding anti-adipocyte monoclonal antibody light chain, Antibody; adipocyte; heavy chain; light chain; obesity; FAT; heart disease; complementarity determining region; CDR; ss. Query Match 82.2%; Score 273.8; DB 2; Length Best Local Similarity 88.9%; Pred. No. 7.6e-76; Matches 296; Conservative 0; Mismatches 37; Indels Trogangagaccogerrance 333 Disclosure; Page 140-141; 182pp; English (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. BP. AAS03477 standard; cDNA; 330 11-OCT-2000; 2000WO-GB003900 99US-0158812P. (first entry) Edwards BM, Main SH, WPI; 2001-282031/29. P-PSDB; AAU02577. WO200127279-A1. 12-OCT-1999; 29-AUG-2001 19-APR-2001 121 241 301 AAS03477; RESULT 8
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light chain coding sequences of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself.

Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel. Fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat heavel as can also be produced e.g. intra- abdominal fat associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 330 BP; 70 A; 102 C; 82 G; 76 T; 0 U; 0 Other;
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Gaps

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Match 80.8%; Score 269.2; DB 4; Length 330; Local Similarity 88.5%; Pred. No. 2.1e-74; es 292; Conservative 0; Mismatches 38; Indels 0

Query Match

Best Loca Matches

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Sequence 330 BP; 69 A; 101 C; 83 G; 77 T; 0 U; 0 Other;

9 60 120 120 180 180

Compared to the present anti-adipocyte monoclonal antibody heavy and light chain coding sequences of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself.

Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The artibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an almost of treatment for obese patients other than undergoing surgery to remove excess fat, Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with

Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related

WPI; 2001-282031/29. P-PSDB; AAU02620.

Disclosure; Page 167; 182pp; English

diseases

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CAGGCTGAGGATGAGGCTGATTATTACTGCAGCTCATATGCAGGCAACGACGAGGTGTGCTT 300
                                                                                                                                                                                                                                 CAGGCTGAGGACGAGGCTGATTATTACTGTTGATATACAACCAGTAGCACTTTGTTA 300
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monoclonal antibody; MAb; vaccine; therapy; ss.
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                                                                                                                                   CACCCAGGCAAAGCCCCCAAACTCATGATTTATGAGGTCAATAAGCGCCCCTCAGGGGTC
                                                                                                                                                                        TERBATEGETTETETEGETECAGETETGGCAACACGGCTECETGTGACCATETETGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody GP44 light chain (V kappa 2) coding sequence.
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                                                                                                                                                                                                                                                                                          TTCGGAAGAGGGACCCGGTTGACCGTCCTA 330
                                                                                                                                                                                                                                                                                                                                                                                              AAQ55659 standard; cDNA; 333 BP
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{first entry}
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22-JUL-1994
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(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY,

2000WO-GB003900 99US-0158812P

11-OCT-2000; 12-OCT-1999;

19-APR-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with HIV-1 gpl20 glycoprotein variants containing the amino acids Asn88, Lys117, Asn262 and Tyr 435 but exhibit at least 50% reduced reacion with gpl20 variants in which these amino acids have been deleted or substituted. The MAD's are useful for passive immunotherapy and their anti-idiotypic antibodies can be used in the production of vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                   Monoclonal antibodies to HIV-1 - directed against glyco:protein gp120, useful for passive immunotherapy or prodn. of anti-idiotype vaccines.
                                                                                                                                                                                                                                                                                                                                                     The monoclonal antibodies (MAb's) designated GP13, GP44 and GP68 react
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGTCTGCCCTGACTCAGCCTCCCTCCGGGTCTCCTCGGACAGTCAGCACCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 79.8%; Score 265.8; DB 2; Length 333; Local Similarity 87.4%; Pred. No. 2.5e-73; es 291; Conservative 0; Mismatches 42; Indels 0.
                                                                                                                              'note= "Framework IV. J lambda 2 segment."
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 333 BP; 69 A; 104 C; 81 G; 79 T; 0 U; 0 Other;
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                          *tag= a
'note= "Encodes CDR 1."
154. .174
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note= "Encodes CDR 2."
71. .294
                                                                                      /*tag= c
/note= "Encodes CDR 3."
         cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 17-18; 34pp; English.
                                                                                                                                                                                                                                (NEWE-) NEDERLANDEN MIN WELZIJN
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                                                                                                          307. .342
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                                                                                                                      *tag=
                                                                                                                                                                                                                                                                      WPI; 1994-036603/05.
                                                                                                                                                                                                                                                                                                                                                                                                                          correct PA field.)
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                misc_feature
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The present invention relates to a specific binding member which binds human glycoprotein VI (GPVI), comprising an antibody VH domain and/or an antibody VH domain. The antibody VH domain comprises 18B12 VH domain, IC3 VH domain or a VH domain comprising a VH CDR3 or optionally one or more VH CDR. The specific binding and VH CDR3 or optionally one or more VH CDR. The specific binding mamber is useful for the manufacture of a medicament for treating a disease or disorder comprising cardiovascular conditions, thrombosis, stroke, intermittent claudication, conditions with disseminated intravascular coagulation, thrombocytopenic purpura, haemolytic ursemic strokes, intermittent claudication, conditions with disseminated intravascular coagulation, thrombocytopenic purpura, haemolytic ursemic syndrome, damage to blood vessel wall resulting from surgery or therapy, collagen-induced inflammation, homozygous sickle disease, kidney damage collagen-induced inflammation, homozygous sickle disease, kidney damage collagen-induced inflammation, nemperance is a coding sequence of an angiopathic vasculitides. The present sequence is a coding sequence of an antibody domain shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New specific binding member binding human glycoprotein VI (GPVI) and comprising an antibody VH domain and/or an antibody VL domain, useful for the manufacture of a medicament for treating a disorder, e.g., thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TCCTGCACTGGAACCAGCAGTGACGTTGGTTATAACTATGTCTCCTGGTACCAACAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, antibody, glycoprotein VI, GPVI, 10B12, 1C3; variable heavy, variable light; CDR; platelet aggregation; cardiant; thrombolytic; cerebroprotective; antisickling; vasotropic; cardiovascular disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Human glycoprotein VI antibody 1C3 variable light chain DNA.
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11 Similarity 87.3%;
288; Conservative (
ACC85452 standard; DNA; 330
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                                                                                                                                                                                                                                                                                      (first entry)
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P-PSDB; ABR63614.
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                                                                                                                                                                                                                                                                                                                                                                                                                  241 CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATTTGCGAACAGCGGCCC---CTTA
  61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
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                                                                                                                                                                          CAGGCTGAGGAGGCTGATTATTACTGCAGTTCATATACAGGCAGCAGCACCACTTGGGTG 300
1; SCA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for inhibiting the formation of aggregates of certain proteins, involving contacting the procein with a binding molecule known as an intrabody. Proteins to be bound include those associated with neurological disorders, and so the method can be used in the prevention of diseases such as Alzheimer's, Parkinson's and Huntington's diseases, prion disease, frontotemporal dementia, amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy, dentacorubal-pallidoluyaian atrophy, spinocerebellar ataxia type 1 (SCA1), SCA2, SCA3, SCA5, SCA6 and SCA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting intracellular polypeptide accumulation, useful for treating neurological disorders, e.g. Alzheimer's disease, comprises contacting the polypeptide with a specific intrabody.
                                                                                          rerancecrirererederecaagrergacaacaacaccereceacareregeere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurological disorder, Huntington's disease, Alzheimer's disease, Parkinson's disease, prion disease, frontotemporal dementia; supvotrophic lateral sclerosis; spinal and bulbar muscular atrophy, denterorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1; SCA3; SCA4; SCA5; SCA7; protein accumulation; intrabody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.6%; Score 248.4; DB 4; Length 327;
larity 86.7%; Pred. No. 7.4e-68;
Conservative 0; Mismatches 41; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huntingtin minimal sPv binding region coding sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 327 BP; 64 A; 102 C; 79 G; 82 T; 0 U; 0 Ocher;
                                                                                                                                                                                                                                          TICGGAAGAGGACCCGGITGACCGICCIA 330
                                                                                                                                                                                                                                                                         TTCGCCGAGGACCAAGGTCACCGTCCTA 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUL-1999; 99US-0146047P.
21-JUL-2000; 2000US-00620955.
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                                                                                                                                                                                                                                                                                                                                                                                                               AAF58706 standard; DNA; 327
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(LECE/) LECERF J.
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Best Local Similarity
Matches 286; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-182700
P-PSDB; AAB69602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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AAFS 8707

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Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor antagonists.
                                                             /*tag= a
/product= "Human KDR (VBGFR-2) Fab light chain (VL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of inhibiting tumour growth which
                                                                                                                              protein"
/note= "CDS does not include start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; Page 125; 151pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        04-MAR-2002; 2002WO-US006762.
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                                                                                                                                                                                     /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCL-) IMCLONE SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ROCK/) ROCKWELL P. (GOLD/) GOLDSTEIN N I.
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P-PSDB; AAE28872.
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Gaps

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(VEGER) antagonists in combination with radiation, chemotherapeutic agent, or epidermal growth factor receptor (BGER) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spieen, bone, kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, bone arrow, blood, thymus, uterus, testicles, cervix or liver) over expresses vGCFR. It is also useful for inhibiting growth of colon tumour or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR. It is preferably useful for treating subjects with both solid tumours, preferably high vascular tumours and non-solid tumours. The inhibition or reduction of tumour growth includes prevention or inhibition of the progression of tumour including cancerous and non-cancerous tumours, where the progression of tumours includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is human KDR (VEGFR-2) Fab antibody light chain DNA
administering, vascular endothelial growth factor receptor
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Sequence 330 BP; 73 A; 104 C; 72 G; 81 T; 0 U; 0 Other;

The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing proteins block activation of the vector and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leuksemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This polynucleotide sequence represents a human DNA sequence relating to the bispecific antibodies that bind to the VEGF receptors of

New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors.

WPI; 2003-201468/19

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Disclosure; Page 72-73; 98pp; English.

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                                                      CAGECTGCCCCGACTCAGCCTCCCTCTGTGTCTCGGGTCTCCTGGACAGTCGGTCACCATC
                                                                                                             TCCTGCACTGGAACCAGGGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
                                                                                                                                                                CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
                                                                                                                                                                               CACCCAGGCCAAGCACCCAAACTCGTGATTTATGACGGCAATAAGCGGCCCTCAGGAGTT
                                                                                                                                                                                                                                   CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA
                                                                                 caercrececreactresecrecererereservicesecreseacastane
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                            Gaps
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Query Match
73.2%; Score 243.6; DB 6; Length 330;
Best Local Similarity 83.6%; Pred. No. 2.4e-66;
Matches 276; Conservative 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                              TTCGGAAGAGGGACCCGGTTGACCGTCCTA 330
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73.2%; Score 243.6; DB 7; Length 330; 83.6%; Pred. No. 2.4e-66; ive 0; Mismatches 54; Indels 0;

Query Match
Best Local Similarity 83.6%;
Matches 276; Conservative

Sequence 330 BP; 73 A; 104 C; 72 G; 81 T; 0 U; 0 Other;

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TOTGATOGOTTOTOTOGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC TCTAATGGTTCTCTGGCTCCAAGTCTGGGAACAGGGCCTCCCTGAAATCTCTGGACTC

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CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTATACAACCAGTAGCACTTTGTTA 300 cadecreaseaceaecrearratracrecaacrearraracaecaecaecarrararer 300

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TTCGGAAGAGGGACCCGGTTGACCGTCCTA 330 301 Tregaacregeaccaagercaccerecta 330

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Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; human; gene; ds.
                                                                       VEGF binding related DNA SEQ ID No 80.
                 ABT23328 standard; DNA; 330 BP
                                                     (first entry)
                                                     01-MAY-2003
                                    ABT23328;
                                                                                                                             Ношо
        ABT23328
RESULT
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26-JUN-2002; 2002WO-US020332 26-JUN-2001; 2001US-0301299P (IMCL-) IMCLONE SYSTEMS INC.

WO2003002144-A1

09-JAN-2003

tumour, vascular endothelial growth factor receptor; VEGFR, epidermal growth factor receptor; EGFR; cancer; human; ds; gene. Human light chain variable region DNA #3. ADD24421 standard; DNA; 330 (first entry) JS2003108545-A1 15-JAN-2004 Homo sapiens 12-JUN-2003. ADD24421;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TCCTGCACTGGAACCAGGGATGACGTTGGTATAACTATGTCTCCTGGTACCAACAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGATCGCTTCTGGCTCCAAGTCTGGCAACAGGCCTCCCTGACCATCTCTGGGCTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CAGGCTGAGGACGAGGCTGATTACTGATGATCATATACAACCAGTAGCACTTGTTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of inhibiting tumour growth comprising administering to a human a vascular endothelial growth factor receptor (VEGFR) antagonist and epidermal growth factor receptor (REGRI) antagonist. The method is useful for inhibiting tumour growth. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                    Inhibiting tumor growth by administering to a human a vascular endothelial growth factor receptor (VEGFR) antagonist and epidermal growth factor receptor (EGFR) antagonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.2%; Score 243.6; DB 9; Length 330; Best Local Similarity 83.6%; Pred. No. 2.4e-66; Matches 276; Conservative 0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 330 BP; 73 A; 104 C; 72 G; 81 T; 0 U; 0 Other;
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                                  10-FEB-1994, 94US-00196041.
20-OCT-1994, 94US-00326552.
07-MVN-1995, 95US-00476533.
03-SEP-1996, 96US-00706804.
07-JAN-1997, 97US-00779450.
10-NOV-1997, 97US-00967113.
22-SEP-1999, 99US-00401163.
02-MAR-2001, 2001US-00798689.
                                                                                                                                                                                                    Rockwell P, Goldstein NI;
                                                                                                                                                                          GOLDSTEIN N I.
                                                                                                                                                                                                                            WPI; 2003-801265/75.
P-PSDB; ADD24422.
                                                                                                                                                           (ROCK/) ROCKWELL
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04-MAR-2002; 2002US-00091300

Search completed: June 19, 2004, 03:30:41 Job time : 279 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

June 19, 2004, 03:16:57; Search time 63 Seconds (without alignments) 2933.312 Million cell updates/sec US-09-019-441A-1_COPY_58_390 333 1 cagtctgcccgactcagcc......cccggttgaccgtcctaggt 333 Title: Perfect score: Sequence: Run on:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 seqs, 277475446 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 333

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

lssued_Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

۵	Description	201-13 Sequence 13, Appl	11			27	33	ij	A-43 Sequence 43	equence 1	'n	-126 Sequence 120	equence 223	equence 129	128	equence 130	-124 Sequence 124	-123 Sequence	125	-62 Sequence 62,	127 Sequence 127	15,	-15 Sequence 15,	10,	-10 Sequence 10,	28-10 Seguence 10,	80-10 Sequence 1	3-10 Segmenter 10
SUMMERS	0.	-958-	US-08-958-2(US-09-240-2	US-09-240-2	-08-652-		US-08-199-93	08-477-5		08-264-	-09-240-		-09-240-	09-240-	US-09-240-27	19-240-	240-	19-240-	-08-273-	-09-240-2	US-08-259-37	US-08-468-67	US-08-360-12	US-08-450-57	-09-017-6	US-09-014-88	US-08-450-36
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	Query Match Length	333	333	324	312	333	330	330	333	330	333	327	327	327	327	327	327	327	327	312	327	318	318	324	324	324	324	324
фP	Query Match	82.7	82.2	72.0	62.7	57.7	53.6	Ω. 20.	51.9	ö	50.5	σ	49.3		48.3	48.3		•	45.9		ď,	40.9			40.7	•	40.7	40.7
	Score	275.4		239.6	208.8	192	178.6	76	172.8	ø	S	₩.	64		161	Ø	٠	153	153	4	140.2	ø	136.2	135.4	135.4	135.4	135.4	135.4
	Result No.	r=1	7	М	4	S	9	7	89	0	10	11	12	13	7. 7.4	 5	91	17	18	19	20	21			24		56	27

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Sequence 52, Appli Sequence 1, Appli Sequence 9, Appli Sequence 117, Appl Sequence 117, Appl Sequence 28, Appl Sequence 24, Appl Sequence 24, Appl Sequence 120, Appl Sequence 121, Appl Sequence 121, Appl Sequence 1121, Appl Sequence 1121, Appl Sequence 1121, Appl Sequence 50, Appli Sequence 50, Appli Sequence 122, Appli Sequence 122, Appli Sequence 122, Appli Sequence 123, Appli Sequence 124, Appli Sequence 126, Appli Sequence 127, Appli Sequence 127, Appli Sequence 127, Appli Sequence 128, Appli Sequence 128, Appli
US-09-025-769B-52 US-08-29-372A-9 US-08-468-671-9 US-08-47-553A-44 US-08-47-553A-44 US-08-62-284-28 US-08-62-86-28 US-09-240-274-116 US-09-240-274-119 US-09-240-274-120 US-09-240-274-120 US-09-240-274-120 US-09-240-274-120 US-09-240-274-120 US-09-240-274-120 US-09-240-274-120 US-09-240-274-120 US-09-240-274-120 US-09-273-146-70 US-09-025-769B-50 US-09-240-274-122
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ALIGNMENTS

RESULT 1	
US-08-958-201-13	
; Sequence 13, Application US/08958201	
; Patent No. 5977319	
; GENERAL INFORMATION:	
Pritchard, Kevin	
Williams,	
MANT: Johnson, Kevin S	
Specific b	
INVENTION: n	
; NUMBER OF SEQUENCES: 23	
E ADDRESS:	
EE: Marshall O'Tool	
.:	
O	
; STATE: Illinois	
Η.	
; ZIP: 60606-6402	
COMPUTER READABLE FORM:	
i MEDIUM TYPE: Floppy disk	
COMPUTER: IBM PC compatible	
SYSTEM: PC-DOS/MS-DOS	
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)	
2	
; APPLICATION NUMBER: US/08/958,201	
; FILING DATE:	
; APPLICATION NUMBER: US 60/028,897	
9	
; INFORMATION FOR SEQ ID NO: 13:	
SEQUENCE CHARACTERISTICS:	
-	
; TYPE: nucleic acid	
器	
fOPOLOGY: linear	
; INMEDIATE SOURCE:	
CLONE: 1C/2D	
FEATURE:	
NAME/KEY: CDS	
; LOCATION: 1.333	
US-08-958-201-13	
Match 82.7%; Score 275	
Similarity 89.2%; Pred. No. 6.2e-78;	
Indels 0;	Gaps

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                    TCTTGCACTGGAACCAGGGGGTTATAAGTATGTTCTGGTACCAAGAGA
                                                                 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
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 TOCTIGGACTIGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
                                                                                                                                  TCTGATCGCTTCTCGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08958201

Sequence 11, Application US/08958201

Sequence 11, Application US/08958201

GENERAL INFORMATION:

APPLICANT: Pope, Anthony R

APPLICANT: Williams, Andrew J

APPLICANT: Williams, Andrew J

APPLICANT: Williams, Andrew J

APPLICANT: Williams, Specific binding members for estradiol;

ITILE OF INVENTION: Specific binding members for estradiol;

ITILE OF INVENTION: materials and methods

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago

STATE: Illinois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.2%; Score 273.8; DB 2; Length 333; Best Local Similarity 88.9%; Pred. No. 2e-77; Matches 296; Conservative 0; Mismatches 37; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/958,201
FILING DATE:
PRIOR APPLICATION NUMBER: US 60/028,897
FILING DATE:
NPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 Dase pairs
SEQUENCE CHARACTERISTICS:
LENGTH: 333 Dase pairs
STRANDEDNESS: double
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: D12 (light chain)
                                                                                                                                                                                                                                                                           TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
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US-08-958-201-11
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121 CACCCCAGGCAAAACTCATGATTTTTGAGGTCAGTAAATCGGCCCTCAGGGGTT 180

181 TCTGATCGCTTCTGGCTCCAAGTCTGGCAACAGGGCCTCCCTGACCATCTCTGGGCTC

181 CCTAATCGCTTCTCAGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTGGGCTCC

CACCCAGGCAAAGCCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC

241 CAGGITGAGGACGAGGCTGATTATTACTGCAGCTCACTTACACGCAGAGTCACTGGATC 300

TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 333

301

CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300

241

TCCTGCACTGGAACCAGCAGTGACGTTGGTTATAAGTATGTCTCCTGGTACCAACAG 120

61 61 121

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Sequence 137, Application US/09240274

Sequence 137, Application US/09240274

Patent No. 6555455

SEREMAL INFORMATION:
TITLE OF INVENTION: Bh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SOFFING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SOFFING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SOFFING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: NUMBER: US/09/240,274
CURRENT APPLICATION NUMBER: 60/081,380
SARLIER FILING DATE: 1998-04-10
SARLIER FILING DATE: 1998-04-10
SARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFFWARE: PatentIn Ver. 2.0
SEQ ID NO 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 GCCCCCAAACTCCTGACTCATGAGGGCACTAAGCGGCCCTCAGGGGGTCCCTGATCGCTTC 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.0%; Score 239.6; DB 3; Best Local Similarity 86.8%; Pred. No. 1.4e-66; Matches 276; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA; ORGANISM: ORGANISM: PEATURE: PEATURE: OFFICE INFORMATION: anti-Rh(D) chain R01US-09-240-274-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 ACCCGGTTGACCGTCCTA 330
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US-09-240-274-137
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GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: EACH INFORMATION: APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: SCRTING METHOD FOR PRODUCTION THEREOF
TILE REPERENCE: 09596-42U2
CURRENT APPLICATION WHRER: 10599-01-294
CURRENT APPLICATION NUMBER: 60/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PECELIN Ver. 2.0
IENGTH: 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 208.8; DB 3; Length 312;
Pred. No. 8e-57;
0; Mismatches 37; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: Obbourn, JK
APPLICANT: Allen, DJ
APPLICANT: MCLEFELY, JG
TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borning members.
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6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: anti-Rh(D) chain S01
US-09-240-274-138
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STATE: Illinois
COUNTRY: United States of America
                                        Sequence 138, Application US/09240274
Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 ACCCGGTTGACCGTCCTA 330
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Best Local Similarity 83.6%;
Matches 266; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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Illinois
RESULT 4
US-09-240-274-138
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US-08-652-816A-27
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61 TCCTGCTCTGGAAGCACCCCCAACAT---TGGAATAATATTGTCTCCTGGTACCAACAG 117
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
CURRENTED: PATENTIN Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/52,816A
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 952004.9
FILING DATE: 23-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 33-MAY-1996
FILING DATE: 07-DEC-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 10-DEC-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 10-UN-1994
ATTORNEY APPLICATION NUMBER: US 08/244,597
FILING DATE: 10-UN-1994
ATTORNEY APPLICATION NUMBER: 28 111/33308
TELEBHONE: 312-414-6300
INFORMATION FOR EQ 1D NO: 27:
ERERERNEY CHARACTERISTICS:
ELENDANT: CACIOGRA
TELEBHONE: 313-444-6300
INFORMATION POR EC 10 NO: 27:
ELEBUSHING CACIO NO: 27:
ELEBUSHING CACIO NO: 27:
ELEBUSHING CACIO ACCIOUNTED CACIO
TELEBHONE: 313 DASSE PAIRS
ELEBUSHING CACIO NO: 27:
ELEBUSHING CACIO ACCIOUNTED CACIO
TELEBHONE: 313 DASSE PAIRS
ELEBUSHING CACIO ACCIOUNTED CACIO
TELEBHONE: 313 DASSE PAIRS
ELEBUSHING CACIO ACCIOUNTED CACIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 TTATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 333
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nucleic acid
BDNESS: double
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Best Local Similarity 77.44
Matches 260; Conservative
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61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CAGTCTGCGTTGACGCAGCCGCCTCAGTATCTGCGGCCCCAGGAAGGTCACCATC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CAGITTGCCCCCGACTCAGCCICCTCTGTGTCTCCTGGACAGTCGGTCACCAIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.9%; Score 176.2; DB 1; Length 330; 74.8%; Pred. No. 1.8e-46; Live 0; Mismatches 78; Indels 6
                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: B-lymphocyte
CELL LINE: 123AV16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_binding 67..106
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152.173
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270..303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: 123AV16-1
FEATURE:
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FEATURE:
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LOCATION:
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FRATURE:
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US-08-199-911-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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                                                             Sequence 132, Application US/09240274

Patent No. 6555455

GENERAL INFORMATION:
TITLE OF INVENTION: EACH NO. FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

SARIER PLING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 GCCCCCAAACTCGTCATCTACAATGACAACAATGGGCCCTCAGGGGTCCCTGACGGTTC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 TCTGGCTCCAAGTCTGGCACCTCCTGGCCATCACTGGCTCAGGCTGAGGAT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 ACCAGGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCACCCCAGGCAAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTC 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Sequence 1, Application US/08199911
| Sequence 1, Application US/08199911
| Patent No. 5495002
| GENERAL INFORMATION:
| APPLICANT: Kobrin, Barry J.
| APPLICANT: Haspel, Mattin V.
| TITLE OF INVENTION: Tumor Associated Monoclonal Antibody
| TITLE OF INVENTION: 123AV16
| NUMBER OF SEQUENCES: 4
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: AKZO NOBEL
| STREET: 1330 Piccard Drive
| STREET: Maryland
| STREET: Waryland
| STREET: Waryland
| STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.6%; Score 178.6; DB 3; Length Best Local Similarity 74.5%; Pred. No. 3.1e-47; Matches 239; Conservative 0; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: anti-Rh(D) chain 001
US-09-240-274-132
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                 RESULT 6
US-09-240-274-132
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US-08-199-911-1
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Sequence 134, Application US/09240274

Patent No. 6255455

James Information

APPLICANT: Siegel, Donald L.

APPLICANT: Siegel, Donald L.

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SONTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SONTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SONTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: 1099-04-20

CURRENT APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER FILING DATE: 1998-04-10

MUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 134

LENGTH 330
                                              121 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGGTC 180
                                                                                                                CTCCCAGGAACAGCCCCCAAACTCCTCATTTATGACAATAAAGCGACCCTCAGGGATT 177
                                                                                                                                                                                                                                                                                                  178 cereaceariterereserecaastereseacareaceaceaceresearataces
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                                                                                                                                                                                                                                                                                                                                                                                           241 CAGGCTGAGGAGGCTGATTATTACTGTTCAT---ATACAACCAGTAGCACTTTG
                                                                                                                                                                                                                       TOTGATOGCTTCTTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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Pred. No. 3.4e-44;
0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 GIGITICGCCGGAGGGACCAAGCTGACCGTCCTAAGT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 TTATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 333
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; OTHER INFORMATION: anti-Rh(D) chain 003
US-09-240-274-134
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Best.Local Similarity 74.4%;
Matches 230; Conservative
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ORGANISM: Homo sapiens
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                                                                                        CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
                                                                                                                                                          178 CCTGACCGATTCTCTGGCTCCAAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTC 237
                                                                                                                                                                                                                                                            241 CAGGCTGAGGAGGCTGATTATTACTGTTGTTCAT---ATACAACCAGTAGCACTTTG 297
                                                                                                                                                                                                                                                                                                                                            238 cadacideseaceaesecceariarracieceeaacareesaraccaeacrececeeres 297
TICCCAGGGACAGCCCCCAAACTCCTCATITAIGACAATAATAAGCGACCCICAGGGTT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGTOTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAGTCTGTGTTGACGCAGCCGCCCTAGTGTCTGCGGCCCCCAGGACGACAGAAGGTCACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,553A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
FILING DATE: 23-JUNE-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 8925590.5
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Meth. Donna M.
REGISTRATION NUMBER: 36,607
REGISTRATION NUMBER: 36,607
REGISTRATION SAG-6620
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQUENCE: CHARACTERISTICS:
CH
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US-08-477-553A-43

Sequence 43, Application US/08477553A

Patent No. 5919910

Patent No. 5919910

Patent No. Formary HUGHES-UNES, Nevin C

TITLE OF INVENTION:
NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:
ADDRESSES: ADDRESSES:
ADDRESSES: ADDRESSES:
CORRESPONDENCE ADDRESS:
STREET: VO. Box 1404

CITY: Alexandria
STREET: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                     298 TTATTCGGAAGAGGACCCGGTTGACCGTCCTA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 GTGTTCGGCGGACCAAGCTGACCGTCCTA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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US-08-477-553A-43
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) OTHER INFORMATION: anti-Rh(D) chain LOS
US-09-240-274-126
Sequence 126, Application US/09240274 Patent No. 6255455 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-240-274-223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 cengacegarnerengeendeaagrengeeacereaecerecengseeareagaere 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGAT---ATACAACCAGTAGCACTTTG 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 cagrereacearcacercarrarrarrenereceacearcaceacecercaaagerere 297
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                                          Sequence 5, Application US/08264093

Sequence 5. Application US/08264093

GENERAL INPORMATION:
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIONA SURFACE TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 230 Richmond-Adelaide Centre
STREET: 230 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.5%; Score 168; DB 1; Length 333; 72.9%; Pred. No. 7.1e-44; Live 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS 6.00 SOFTWARE: ASCII Editor CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/264,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICALL.
FILING DATE:
FILING TAPPLICATION:
ATTORNEY AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
FREPERING POCKET NUMBER: NOVOP/106A/7551
TELEPONE: (416) 868-1482
TELEPAX: (416) 868-1482
TELEPAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: INCLEIC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 GTATTCGGCGGAGGACCAAGCTGACGTTCTAGGT 333
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Best Local Similarity 72.9
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSH 237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
US-08-264-093-5
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RESULT 11 US-09-240-274-126

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Sequence 223, Application US/09240274

Sequence 223, Application US/09240274

Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09564-220
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT APPLICATION NUMBER: 00/08,380
EARLIER FILING DATE: 1999-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 223

LENGTH: 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 ACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCACCAGGCAAA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGCTGATTATTACTGTTCAT --- ATACAACCAGTAGCACTTTGTTTCGGAAGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REPERRNCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
BARLIER PILING DATE: 1998-04-10
BARLIER PILING DATE: 1998-04-10
BARLIER PILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTY OF ALCOHOLOGY
SAGOTARRE: DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTY OF ALCOHOLOGY
BEQUENT: 1327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 TCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 ACTOAGCCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
49.3%; Score 164.2; DB 3; Length 3
Best Local Similarity 73.8%; Pred. No. 1.1e-42;
Matches 237; Conservative 0; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 128, Application US/09240274
; GENERAL INFORMATION:
; APPLICANT: Stepel, Donald L.
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REPRENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT PILING DATE: 1999-01-29
; BARLIER PILING DATE: 1998-04-10
; BARLIER PILING DATE: 1998-04-10
; BARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; FEBRENCE: 2.0
                                                                                                                                                                                                                       253 GAGGCTGATTATTACTGTTGTTCAT---ATACAACCATAGCACTTTGTTATTCGGAAGA 309
247 GAGGCTGATTATTACTGTGCGGCATGGGATGACAGCCTGAGTGCCGTGGTATTCGGCGGA 306
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US-09-240-274-128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 GGGACCAAACTGACGTCCTA 327
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US-09-240-274-130
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Facetant No. 6255455

GENERAL INFORMATION:
FAPLICANT: Siegel, Donald L.
TILLE OF INVENTION:
FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DAME: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DAME: 1998-04-10

EARLIER FILING DAME: 1998-04-10

EARLIER FILING DAME: 1998-01-29

FARIER FILING DAME: 1998-01-01

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PAPELICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

LENGTH: 327
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                                                                                                                                                                                        Score 164.2; DB 3; Length
Pred. No. 1.1e-42;
0; Mismatches 78; Indels
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Pred. No. 3.7e-42;
0; Mismatches 79;
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH55
US-09-240-274-223
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US-09-240-274-129
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Best Local Similarity 73.5%;
Matches 236; Conservative C
                                                                                                                                                                                             Query Match
Best Local Similarity 73.8%;
Matches 237; Conservative
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253 GAGGCTGATTATTACTGTTCAT---ATACAACCAGTAGCACTTTGTTATTCGGAAGA 309 73 ACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCACCCAGGCAAA 132 10 AGCAGCTCCAACATTGACAG---TAACTATGTATCCTGGTACCAGCAGCTCCCAGGAAGA 126 133 GCCCCCAAACTCATGATTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATGGCTTC 192 127 GCCCCCAAACTCCTCATTTTGACAATTATAAGGGACCCTCAGGAATTCCTGACCGATTC 186 193 TCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGAC 252 187 TCAGGCTCCAAGTCTGGCACGTCCAGCCACCCTGGGCATCACGGGACTCCAGACTGGGGAC 246 247 GAGGCCGATTATTACTGTGCAACATGGGATGACAGCCTGAATGGTCGGGGTGTTCGGCGGA 306 APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REPERENCE: 09596-402
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-10-29
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PECENTIN VET. 2.0
ENGINE NO 130
LENGTH: 327 13 ACTICAGCTTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGGA 72 10 ACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGATCACCATCTCCTGCTGAA 69 6; Gaps Query Match

48.3%; Score 161, DB 3; Length 327;
Best Local Similarity 73.2%; Pred. No. 1.2e-41;
Matches 235; Conservative 0; Mismatches 80; Indels TYPE: DNA ORGANISM: Homo sapiens PEATURE: OTHER INFORMATION: anti-Rh(D) chain N01 US-09-240-274-130 310 GGGACCCGGTTGACCGTCCTA 330 G G à 쉱 8 6 8 6 हे ò

Search completed: June 19, 2004, 04:31:43 Job time : 64 sece

307 GGGACCAAGCTGACCGTCCTA 327

Sequence 11, Appl Sequence 22, Appl Sequence 27886, Appl Sequence 3, Appli Sequence 18427, A Sequence 18429, A

Sequence

1926, Ap 1926, Ap 1926, Ap 1926, Ap 1934, App 134, App 126, App 127, App 129, App 129, App 129, App 129, App

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APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: He, Yudong
APPLICANT: Ho, Yudong
APPLICANT: Mao, Mao, Mao
APPLICANT: None: Laura Johanna
APPLICANT: None: Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Parnada, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999 and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999 18
FILE REPRICATION NUMBER: 60/298,918
FRIOR APPLICATION NUMBER: 60/298,918
FRIOR APPLICATION NUMBER: 60/298,710
FRIOR APPLICATION NUMBER: 60/298,710
FRIOR FILING DATE: 2002-06-18
FRIOR FILING DATE: 2002-06-18
FRIOR FILING DATE: 2002-06-14
FRIOR FILING DATE: 2002-06-14
FRIOR FILING DATE: 2002-06-14
                                         US-09-734-613-22
US-09-864-761-27886
US-10-199-908-3
US-10-199-918-95-18429
US-10-99-918-995-18429
US-10-99-18-995-18429
US-10-091-300-40
US-10-98-88-798-132
US-10-091-300-46
US-10-091-300-46
US-10-091-300-48
US-10-091-300-48
US-10-091-300-48
US-10-091-300-48
US-09-848-798-126
US-09-848-798-128
US-09-848-798-125
US-09-848-798-125
US-09-848-798-125
US-10-155-437-3
US-09-848-798-127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 200, Application US/10342887
Publication No. US20040058340AI
GENERAL INFORMATION:
 ; TYPE: DNA; CORGANISM: Homo sapiens
US-10-342-887-200
US-10-342-887-200
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168.2
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164.2
162.6
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155.4
153.6
 Sequence 200, App
Sequence 200, App
Sequence 96, Appl
Sequence 14141, A
Sequence 28, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 1224, A
Sequence 1524, A
                                                                                                    June 19, 2004, 03:26:07; Search time 284 Seconds (without alignments) 5371.489 Million cell updates/sec
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                                                                                                                                                                                                     1 cagtotgccccgactcagcc......cccggttgaccgtcctaggt 333
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_RMF PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/PCT_RMF PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_NUB_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US06_NUB_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NUB_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NUB_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_NUB_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NUB_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09_NUB_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US09_NUB_PUB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US09_NUB_PUB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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3 US-10-172-118-200
10 US-10-39-518-200
7 US-10-63-244-86
5 US-10-063-244-86
5 US-10-029-386-14141
5 US-10-091-300-28
6 US-09-848-798-137
0 US-09-879-813-85
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0 US-09-879-813-85
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0 US-09-874-613-85
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0 US-09-734-613-15
3 US-09-734-613-15
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                                                                                                                                                                                                                                                                                 3017426 seqs, 2290544650 residues
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Maximum Match 1008
Listing first 45 summaries
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Maximum DB seq length: 333
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Match
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Perfect score:
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Query Match
85.5%; Score 284.6; DB 13; Length 331;
Best Local Similarity 91.2%; Pred. No. 4.4e-87;
Matches 302; Conservative 0; Mismatches 29; Indels 0;

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241 CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCACTCGGGTG 300
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                                                                                                                                                                                                  Sequence 96, Application US/10399518
Publication No. US20040091475A1
GENERAL INFORMATION:
APPLICANT: TSUGHIYA, MASAVUXI
APPLICANT: OFFICHINA
APPLICANT: YABUTA, NAOHIRO
APPLICANT: YABUTA, NAOHIRO
APPLICANT: TSUNODA, HIROYUXI
APPLICANT: TSUNODA, HIROYUXI
APPLICANT: OFFICANION UNDERSADED TPO AGONIST ANTIBODY
TITLE OF INVERTION: DEGRADED TPO AGONIST ANTIBODY
TITLE OF INVERTION: DEGRADED TPO AGONIST ANTIBODY
FILE REFERENCE: 065678/0111
CURRENT APPLICATION UNDERS: 102/10/399,518
CURRENT APPLICATION NUMBER: PCT/JP01/03288
PRIOR FILING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
PRIOR PLING DATE: 2001-09-12
PRIOR PLING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PATENTING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 183
SEQ ID NO SEQ ID NOS: 183
LENGTH: 330
                                            301 TTCGGAAGAGGGACCCGGTTGACCGTCCTAG 331
                                                                        301 TICGGCGGAGGACCAAGCTGACCGTCCTAG 331
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APPLICANT: Rondon, Isaac J.; APPLICANT: Rege, Albert; APPLICANT: Rent, Rachel Baribault; TITLE OF INVENTION: CD44 LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Mus sp.
US-10-399-518-96
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                                                         61 TCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACCATGTCTCCTGGTACCAACAA 120
                                                                                                                CACCCAGGCAAAGCCCCCCAAACTCATGATTTATGATGTCGCTAAAGCGGGCCTCAGGGGTC 180
                                                                                                                                                                                                         TCTGATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
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APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mac, Mac
APPLICANT: Roberts, Chris
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTIONS Diagnosis and Prognosis of Breast Cancer Patients
FILE REPERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: 60/206-14
FRICH APPLICATION NUMBER: 60/380,770
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR PILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 200
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                                                                                                                                                                                                                                                                                                                                                                                               TICGGAAGAGGACCCGGTTGACCGICCTAG 331
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Publication No. US20030224374A1
GENERAL INFORMATION:
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DATABASE ACCESSION NUMBER: AJ249377
DATABASE ENTRY DATE: 2001-06-18
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ORGANISM: Homo sapiens
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US-10-172-118-200
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Matches 302;
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RESULT 6
US-10-091-300-28
US-10-091-300-28
Sequence 28, Application US/10091300
Publication No. US20030108545A1
GENERAL INFORMATION:
APPLICANT: ROCKWell, Patricia
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular TITLE OF INVENTION Endothelial Growth Factor Receptor Antagonist
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT PILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8:0 for Windows
                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                               121 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTGGCTAAGCGGCCTCAGGGGTC 180
163 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGAGGGCAGTAAGCGGCCCTCAGGGGTF 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 cadecidadeaceagecteatrarractecaacteararetaageageagerrirarsic 300
                                                                                                                                                                                            283 CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATC
                                                                                                                                                                                                                                                                           223 TCCTGCACTGGAACCAGCAGTGATGTTGGAGTTATAAACCTTGTCTCCTGGTACCAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                            103 TCTAATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC

181 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGAACAACTCTCTGGACTC
                                                                                                                                                                                                                                                  TCCTGCACTGGAACCAGGGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                   181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
                                                                                                                        Gaps
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                                                                             Length 294;
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Pred. No. 5.1e-73;
0; Mismatches 54; Indels 0;
           ; OTHER INFORMATION: EST_HUMAN HIT: BG754419.1, EVALUE 0.00e+00 US-10-029-386-14141
                                                                          Score 245.2; DB 15; Length Pred. No. 1.4e-73; O: Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 CAGGCTGAGGACGAGCTGATTATTACTGCTGCTCCATATGCA 2
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                                                                          Query Match
Best Local Similarity 91.8%;
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.6%;
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Human
US-10-091-300-28
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LENGTH: 330
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Publication No. US2033194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: HORAR DAVIG R.
TITLE OF INVENTION: HUARA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CITLE OF INVENTION: HUARA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CIREMIT APPLICATION NUMBER 105 2001-12.20
NUMBER OF SEO ID NOS: 34288
SOURENT FILING DATE: 2001-12.20
SUPMER OF SEO ID NOS: 34288
SUPMER OF SEO ID NOS: 34288
SUPMER OF SEO ID NOS: 34288
SEQ ID NO 14441
SEQ ID NO 14441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 AACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCACCAGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 GACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGG
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0
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81.4%; Score 271; DB 17; Length 319;
Best Local Similarity 90.6%; Pred. No. 2e-82;
Matches 289; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
PGRANISM: Homo sapiens
PERJUNE:
OTHER INFORMATION: MAP TO CHR22_155.0
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.52
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: NAT HIT: ZSB032.1, EVALUE, O.006+00
OTHER INFORMATION: WHISSPROT HIT: P01705, EVALUE 3.006-47
                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetically generated oligonucleotide US-10-663-244-86
FILE REFERENCE: 10280-063001
CURRENT APPLICATION NUMBER: US/10/663,244
CURRENT FILING DATE: 2003-09-15
FRIOR FILING DATE: 2002-09-15
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PELSON 165
SOFTWARE: 885ESEQ for Windows Version 4.0
SENGTH: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACCAGGCTGACCGTCCTA 319
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                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-029-386-14141/c
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301 TTCGGAACTGGGACCAAGGTCACCTA 330
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RESULT 9 US-09-879-813-85 Š ð d ઠે d ઠે d à d ò Sequence 38, Application US/10091300
Publication No. US20030108545A1
GENERAL INFORMATION NO. US20030108545A1
GENERAL INFORMATION NO. USCOULE OF INVESTION COmbination Methods of Inhibiting Tumor Growth With a Vascular TITLE OF INVESTION: Conditionation Methods of Inhibiting Tumor Growth With a Vascular FILLE REPERBENCE: 11245/46211
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8:0 for Windows
SEQ ID NO 38
LENGTH: 330 CACCCAGGCCCAAAGCCCCCAAAACTCTTGATTAACGATGTCACTAGTCGGCCCTCAGGTGTT 180 240 181 TCTGATCGCTTCTCTGGCTCCAAGTCAGGCCTCACGGCCTCCCTGACCATCTCTGGACTC 240 61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120 61 TCCTGCACCGGCTCCAGCACTGATGTGGGTAATTATAAACTATATCTCCTGGTACCAACAA 120 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180 CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTGTTA 300 241 CAGCCTGAAGACGAGGCTGACTATTACTGCAACTCCTATTCTGCCACCGACACTCTTGTT 300 1 caercracceraacreaceracerecerereresereresereseacaereacere 60 TCTGATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 1 CAGTOTGCCCCCACTCAGCCTCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATC ô Length 330; Query Match 72.7%; Score 242; DB 15; Length 3 Best Local Similarity 83.3%; Pred. No. 1.8e-72; Matches 275; Conservative 0; Mismatches 55; Indels TTCGGAAGAGGGACCCGGTTGACCGTCCTA 330 TITGCCGAGGGACCAAGCTGACCGTCCTA 330 TYPE: DNA ORGANISM: Human RESULT 8 US-09-848-798-137 RESULT 7 US-10-091-300-38 ; ORGANISM: Hu US-10-091-300-38 301, 301 121 121 181 241 d ò g 50 g ठे 셤 8 8 8

RESULT 8
US-09-648-798-137
US-09-648-798-137
Sequence 137, Application US/09848798
Publication No. US20030040605A1
FUBBEAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SOFTING METHOD FOR PRODUCTION THERBOF
FILE OF INVENTION: UNMBER: US/09/848,798
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SENGTH 1374
TYPE: DNA

189 132 70 GCCAGCAGTGACGTTGGTGCTTATAAGCACGTCTCCTGGTACCAACAACACCCCAGGGAAA 129 133 GCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTC 192 193 TCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGAC 252 190 TCTGGCTCCAAGTCTGGCAAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGGCTCAAGAT 249 253 GAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTATTCGGAAGAGGG 312 250 GAGGCTGATTATTACTGCAGCTCATTTGCA---GGTAATTCCGTGATATTCGGCGGAGGG 306 69 73 ACCAGGGATGACGTTGGTGATTATAACTATGTCTCCTGGTACCAACACACCAGGCAAA 130 GCCCCCAAACTCCTGACTCATGAGGGGCACTAAAGGGGCCCTCAGGGGTCCTGATGGTTC 10 ACTCAGCCTCCCTCCGCGTCTCCTGGACAGTCAGTCACCATCTCCTGCACAGGACAGTCAGA 13 ACTICAGOCTICCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGGA ٠. ش DB 10; Length 324; 72.0%; Score 239.6; DB: 86.8%; Pred. No. 1.2e-71. ive 0; Mismatches 33 ; FEATURE: ; CTHER INFORMATION: anti-Rh(D) chain R01 US-09-848-798-137 313 ACCCGGTTGACCGTCCTA 330 307 Accasecratecercicia 324 Query Match 72.0 Best Local Similarity 86.8 Matches 276; Conservative ORGANISM: Homo sapiens

US-09-879-813-85
Sequence 85, Application US/09879813
Sequence 85, Application US/09879813
Sequence 85, Application US/09879813
SERNEAL INFORMATION:
APPLICANT: Sale, Ulian B.
APPLICANT: Sale, Wichael S.
APPLICANT: Cundbers, Sarah J.
ITLE OF INVENTION: Method of Generating Diversity FILE REFERENCE: 18396/2005
CURRENT APPLICATION NUMBER: 2001-06-11
PRIOR APPLICATION NUMBER: 99/828,717
PRIOR PILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: PT/GB99/03358
PRIOR PILING DATE: 1999-10-08
NUMBER: OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.1
SEQ ID NO 85
LENGTH: 300
TYPE: DNA
COGANISM: Homo sapiens
US-09-879-813-85

 Query Match
 71.8%;
 Score 239.2;
 DB 9;
 Length 300;

 Best Local Similarity 89.7%;
 Pred. No. 1.6e-71;
 Geryl;

 Matches 269;
 Conservative 0;
 Mismatches 28;
 Indels 3;
 Gaps

 Qy
 19 CTCCTCCTGTGTGTGTGTGTCTGGACAGTCGGTCACTCCTGGACAGCGGC
 CCTGCCTCCGTGTCTGGGTCTCTGGACAGTCGATCACTCCTGGACAGCGGC
 D

 Db
 1 CCTGCCTCCGTGTCTGGGTCTCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGC
 CAGCCTCCGTGTCTGGGTCTCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGC

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181 TCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGACGACGAGGCT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAACTCATGATTTATGATGTCGCTAAAGCGGGCCTCAGGGGTCTCTGATGGCTTCTCTGGGC 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                     259 GATTATTACTGTTGTTCATATACAACCAGTAGCA----CTTTGTTATTCGGAAGAGGGACC
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89.7%; Pred. No. 1.6e-71;
tive 0; Mismatches 28; Indels
                                                                                                                                                                                                          RESULT 10

US-10-146-505-85

/ Sequence 85, Application US/10146505

/ Publication No. US20030108889A1

/ CENERAL INPORMATION:
/ APPLICANT: Sale, Julian E.
/ APPLICANT: Cumberger, Michael S.
/ APPLICANT: Cumberger, Michael S.
/ TITLE OF INVENTION: Method of Generating Diversity
/ TITLE OF INVENTION: Method of Generating Diversity
/ TITLE OF INVENTION: Method of Generating Diversity
/ FILE REFERENCE: 183-6/2005B
/ CURRENT APPLICATION NUMBER: US/10/146,505
/ CURRENT APPLICATION NUMBER: 09/828,717
/ PRIOR APPLICATION NUMBER: 09/828,717
/ PRIOR FILING DATE: 2001-04-06
// PRIOR FILING DATE: 1999-10-09
// PRIOR PILING DATE: 1999-10-09
// PRIOR FILING DATE: 1999-01-19
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Best Local Similarity 89.73
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-10-146-505-85
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APPLICANT: Hanzel, bavid R. A. TILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY NICROARRAY TILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY GENERAL APPLICATION WORSER: US/0.2014.56

PRIOR APPLICATION WORSER: US/0.2014.66

PRIOR PRIOR PARTICATION WORSER: US/0.2014.66

PRIOR PRIOR CATION WORSER: US/0.0014.0130

PRIOR PRIOR CATION WORSER: PC/10014.0066

PRIOR PLICATION WORSER: PC/10014.0066

PRIOR PL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGCCTCCGFGTCTCGCTGGACAGTCGATCACCATCTCCTGCACTGGAACCAGCA
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OTHER INFORMATION: MAP TO AC002308.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BALN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN HEARINE, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN FATAL LIVER, O.0004-00

OTHER INFORMATION: BST HYMAN HIT: MA405481, EVALUE 0.0004-00

OTHER INFORMATION: SWISSPROT HIT: P01705, EVALUE 4.000-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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Sequence 22661, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION: APPLICANT: Pern, Sharron G.

US-09-864-761-22661

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53 TCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGT 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 ACCAACACCACCCAAGGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 ACCAACAGGACCCCAAAAGCCCCCAAACTCATGATTTATGAGGTCAGTAATGGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 CAGGGGTCTCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 TCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGT
US-09-734-613-15

| Sequence 15, Application US/09734613
| Publication No. US20020088016A1
| Publication No. US20020088016A1
| GENERAL INFORMATION:
| APPLICANT: BRUGGEMANN' MATIANNE
| TILE REPERENCE: 37945-009
| FILE REPERENCE: 37945-009
| CURRENT APPLICATION NUMBER: US/09/734,613
| PRICR APPLICATION NUMBER: US/09/734,613
| PRICR PILING DATE: 1999-11-03
| PRICR PILING DATE: 1999-11-03
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 15
| LENGTH: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-734-613-16
US-09-734-613-16
US-09-734-613-16
Sequence 16, Application US/09734613
Publication No. US20020088016A1
GENERAL INFORMATION:
APPLICANT ERUGGENAN, Marianne
TILL REFERENCE: 37945-0009
CURRENT APPLICATION: UNMERR: US/09/734,613
CURRENT PILIMG DATE: 2000-12-13
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1998-11-03
NUMBER: OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LEMOTTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.6%; Score 218.4; DB 13; Length 246; Best Local Similarity 93.4%; Pred. No. 2e-64; Matches 228; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 64.5%; Score 214.8; DB 13; Length 243; Best Local Similarity 93.0%; Pred. No. 3.4e-63; Matches 225; Conservative 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-734-613-16
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242 CTCT 245
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    AACTCATGATTTATGATGTGCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCTCTGGCT 199
                                                                                                                                                        200 CCAAGICIGGCAACACGGCCICCCIGACCAICICIGGGCICCAGGCIGAGGACGAGGCIG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 TCCTGCACTGGAACCAGCAGTGATGTTGGGAGTTATGACTATGTCTCCTGGTACCAACAG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TCTGATOGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGATCGTTTCTCTGGCTCCAAGTCTGGCAATACGGCCTCCATGACCATCTCTGGACTC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAGICTGCCCCGACTCAGCCICCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACATC
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN MAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
OTHER INFORMATION: SWISSPROT HIT: P01709, EVALUE 1.00e-30
OTHER INFORMATION: NT HIT: X57825.1, EVALUE 0.00e-00
US-10-029-386-15224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 219.6; DB 15; Length Pred. No. 8.1e-65; 0; Mismatches 29; Indels
                                                                                                                                                                                                                                     CAGGCTGAGGACGAGGCTGATTATTA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.9%;
Best Local Similarity 89.1%;
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                      140
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13 RESULT

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172

61

121

232

181

112 CAGGGGTTTCTGATCCTTTCTGGGTCCAAGTCTGCCAACAGGCCTCCTGACCATCT 232 CTGGGCTCCAGGCTCAGGACAGGCTGATTATTACTGTTGTTCATACAACCAGTAGCA 292 61 Gaps 0; Query Match
Best Local Similarity 91.4%; Pred. No. 1.1e-61;
Matches 223; Conservative 0; Mismatches 21; Indels 0; 233 (173 122 6 6 6 6 6 6 6

182 (293

Search completed: June 19, 2004, 04:36:35 Job time: 285 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: Title: Perfect score: Sequence:	June 19, 2004, 03:12:07; Search time 1733 Seconds (without alignments) 5738.088 Million cell updates/sec US-09-019-441A-1_COPY_58_390 333 1 captotacccqactcaqcccccqqttqaccqtcctaqqt 333
Scoring table: IDENTITY NUC Gapop 10.0	IDENTITY NUC Gapop 10.0 , Gapext 1.0

10684158 Total number of hits satisfying chosen parameters:

27513289 seqs, 14931090276 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 333

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database :

1: em_estba:*
2: em_estbum::*
4: em_estbum::*
5: em_estcu::*
7: em_estcu::*
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24: em_gss_liv::*
25: em_gss_liv::*
26: em_gss_liv::*
27: em_gss_liv::*
28: gb_gss_li::*
29: gb_gss_l::*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		CD707555 EST24082	BU584333 3392316H1	BU584280 3045436H1	CD705383 BST21910
		ID		14 CD707555	BU584333	13 BU584280	CD705383
		8	1	4	73	13	14
		Match Length DB		325	280	258	248
p	Query	Match		71.4	69.5	67.4	0.99
		Score		237.6 71.4	231.4	224.4	219.8
	Result	No.		-	01	m	47*

ST2086 RC0-H BST20 BST15 BST307 BST315	463326 573 555980 180 463341 182 UI-HF- 257 BX2832 508 583795	440000	34 30567 55 EST107 55 29210 55 29210 55 29469 51 30469 52 33922 52 3922 52 19605 57 MR4-U	94254 287756 4410 165935 37310 U1-HF- 44379 381475- 99773 B94297 39470 X-BS163 2574 BS1909 2574 BS1909 2674 G10217- 44640 610217- 99335 BP4293
T27942 BF825613 CD703527 CD698983 AA327392 CD698821	8447 9447 9448 9718 9325	BE706848 BU584244 CD695826 BU584067 N47367 BP431103		BUS84254 BUS84110 BUS84110 BUS84310 BUS84273 BUS84279 BUS82400 CD692574 BUS8640 BUS8640
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		50000000000000000000000000000000000000		0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.
217.6 215.6 214.8 213.8 212	22.22.22.22.22.22.22.22.22.22.22.22.22.	00.00.00	1991.2 1891.2 1899.3 189.2 189.8 189.8 189.6 189.6	744 1 1 4 2 6 6 1 1
11 100001	1	222 222 232 243 243 243 243 243 243 243	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	. W W W W W A A A A A A A A A A A A A A

ALIGNMENTS

	CD707555 325 bp mRNA linear BST 25-JUN-2003	EST24082 human nasopharynx Homo sapiens cDNA, mRNA sequence. CD707555	CD707555.1 GI:32238185	BST.	Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 325)	Liu, X Q., Zhou, Y., Zhang, L J., Xu, H., Chen, H K., Pan, Z G. and	Zeng, YX.	Transcriptional Gene Expression Profile of Human Nasopharynx	Unpublished (2003)	Contact: YiXin Zeng	Cancer Center	Sun Yat-sen University	651 DongFeng Road Bast, GuangZhou 510060, China	Tel: 86-1380-9770-743	Fax: 86-20-8775-4506	Email: yxzeng@gzsums.edu.cn.	Location/Qualifiers	1325	/organism="Homo sapiens"	$/mol_type="mRNA"$
RESULT 1 CD707555		ACCESSION		KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS		TITLE	JOURNAL	COMMENT							PEATURES	Bource		

61 TCCTGCACTGGAACCAGCGATGACGTTGGTTATAACTATGTCTCCTGGTACCAACAC 120

16 CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATC 75

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                                                                                                                                                             CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATC 60
                                                                                                                                                                                                                                                                                  61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
                                                                                                                                                                                                                                          TCCTGCACTGGAACCAGCAGTGACGTTGGTTATAACTATGTCTCCTGGTACCAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 280)
Collins, J.B., Goward, M.E., Cole, C.G., Smink, i.J., Huckle, E.J.,
Knowles, S., Bye, J.M., Beare, D.M. and Dunham, I.
Re-evaluating Human Gene Annotation: A Second Generation Analysis of Chromosome 22
/db_xref="taxon:9606"
/tissue type="normal nasopharynx"
/tone lib="human nasopharynx"
/note="fSfs="human nasopharynx"
/note="fSfs generated from a normal nasopharynx cDNA
                                                                                                                                       Gaps
                                                                                                                                     ö
                                                                                                         Length 325,
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                                                                                                  Query Match 71.4%; Score 237.6; DB 14; Length Best Local Similarity 94.6%; Pred. No. 7.7e-57; Matches 246; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
Contact: Parzer SR
Contact: Parzer SR
Incyte Genomics, Inc.
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 845 468
Fax: 650 845 5495
Email: spanzer@incyte.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spanzer@incyte.com.
Location/Qualifiers
1. .280
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                         241 CAGGCTGAGGACGAGGCTGA 260
                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGCTGAGGACGAGGCTGA 325
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
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BU584333
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                                                                         ORIGIN
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BUS84280
3045436H1 HEAANOTO1 Homo sapiens cDNA clone 3045436 5', mRNA
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136 CACCCAGGCAAAGCCCCCCAGACTCATCATTACGATGTCAGTAATCGGCCCTCAGGGGTT 195
                                                 181 TCTGATCGCTTCTGGCTCCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
196 TCTAGTCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 255
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1 (bases 1 to 258)

Collins, J.E., Goward, M.E., Cole, C.G., Smink, L.J., Huckle, B.J., Rxonles, S., Bye, J.M., Beare, D.M. and Dunham, I.

Re-evaluating Human Gene Annotation: A Second Generation Analysis of Chromosome 22

Chromosome 22

Chromosome 22

Chromosome 22

Contact: Panzer SR

Incyte Genomics, Inc.

Jal O Portrat Drive, Palo Alto, CA 94104, USA

Tel: 650 845 4682

Fax: 650 845 5495
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181 CAACACGGCCTCCCTGACCGTCTCTGGGCTCCAGACTGAGGATGAGGCTGCTTATTACTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/organism="Homo sapiens"
/db xref="reaxon:9606"
/clone="3045436"
/tissue type="heart"
/clone lib="HRAANOTO1"
/note="heart, coxonary artery, CAD, 46M"
                                                                                                                            Email: spanzer@incyte.com.
Location/Qualifiers
1. .258
                                                                                                                                                                                                                                                                                                                               BU584280
BU584280.1 GI:23258245
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
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1 CAGTCTGCCCCACTCAGCCTCCCTCTGTGTCTGCGTCTCTGGACAGTCGGTCACCATC

Query Match 69.5%; Score 231.4; DB 13; Length 280; Best Local Similarity 92.1%; Pred. No. 4.1e-55; Matches 244; Conservative 0; Mismatches 21; Indels 0;

Š 요 SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

ACCESSION VERSION KEYWORDS

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153
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182 ACGGCCTCCCTGACCATCTNTGGGCTCCAGGCTGAGGACGAGGCTGATTATNACTGCAGC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Venter, JC
Contact: Venter, JC
The Institute for Genomic Research
312 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699423
Fax: 3018699423
Fax: 1018699423
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 TATAACTATGECTCCTCGTACCACACACCACCAGGCAAAGCCCCCAAACTCATGATTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 GAIGTOGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCTCTGGCTACCAAGTCTGGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/db_xref=PATCC (inhost):100584"
/db_xref="taxon:9606"
/clone lib="Human Spleen"
/note="Organ: spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .260
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Best Local Similarity 89.6'
Matches 232; Conservative
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                                                                                                                                         CD705383 28-5-JUN-2003 EST21910 human nasopharymx Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                 Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                 (bases 1 to 248)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol type="mkNa"
/db Azef="taxon:9606"
/tissue[rype="normal nasopharynx"
/clone lib="human nasopharynx"
/nore="ESTS generated from a normal nasopharynx cDNA
library from southern Chinese"
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
1el: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                             241 CTGCTCATTTACAGGCAG 258
                   270 TIGITCATATACAACCAG 287
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CD705383.1 GI:32236013
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61

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CD703527 327 bp mRNA linear EST 25-JUN-2003
EST20054 human nasopharynx Homo sapiens CDNA, mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 327)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. Zeng,Y.-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/note="ESTS generated from a normal nasopharynx cDNA
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                      275 CATATACA --- ACCAGTAGCACTTTGTTATTCGGAAGAGGGACCCGGTTGACCG
                                                         247 CATTIGGAGGACCAACCGCGCTGTGTTTTCGGCGGAGGGACCACGCAGGAAAGG
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Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
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Location/Qualifiers
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CD703527.1 GI:32234157
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
Contact: YiXin Zeng
Cancer Center
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                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (Dases I to 307)

1 (Dases I to 307)

1 Das Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carralho,A.F., Matsuxuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCO&t2=RCO-HN0024-161100-021-g07&t3=2000-11-16&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 307.
                                                      307 bp mRNA linear EST 13-JAN-2001
RCO-HN0024-161100-021-g07 HN0024 Homo sapiens cDNA, mRNA sequence.
BF825613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGTTGTT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 CGGCCTCCCTGACCGTCTCTGGGCTCCAGGCTGAAGATGAGGCTGATTATTACTGCAGCT
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 215.6; DB 10; Length
Pred. No. 1.4e-50;
0; Mismatches 39; Indels
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85.7%;
                                                                                                                                                                                                            Homo sapiens (human)
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Best Local S
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VERSION
KEYWORDS
SOURCE
ORGANISM
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Matches
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AUTHORS
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MEDLINE
PUBMED
RESULT 6
BF825613
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Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.P., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.B., Scott, J.L., Saudek, D.M., Shirley, R. Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, B.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Hudson, P., Kim, A.K., Kozak, D.L., Runsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Parmond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Pannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Vencer, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
L. Nature 377 (6547 Suppl), 3-174 (1995)
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183 TCTNATCGCTTCTNTGGCTCCAAGTNTGGCAACACGGCCTCCTGACCAACAATGGTTT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 TACCCGGGGAAAGNCCCCCGACTCCTGATTTCTGAGGTCAGGAATCGGCCTCAGGGTT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CAGGCTGAGGACGC-TGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTT 299
243 CAGGCTGCAGACGAGGCTTGATTATTACTGCAGAGCGTATTCTTNCACCAGTCCTTGTGT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
Bioinformatics
Bioinformatics
Bioinformatics
First Institute for Genomic Research
7712 Medical Center Drive, Rockville, MD 20850 USA
772 Medical Center Drive, Rockville, MD 20850 USA
773 Medical Center Drive, Rockville, MD 20850 USA
774: 3018699056
First Institute of Center Drive, Rockville, MD 20850 USA
775 Clone availability, additional sequence and expression
776 Clone availability, additional sequence and expression
777 For clone availability, additional sequence and expression
778 For clone availability additional sequence and expression availability additional sequence availability additional sequence and expression availab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol type="mRNA"
/db_Xref="ATCC (inhost):128073"
/db_Xref="teaxon:9606"
/dev_stage="adult"
/clone lib="collon I"
/note="organ: colon, Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: AhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
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64.1%; Score 213.4; DB 9; Length 313;
Best Local Similarity 81.8%; Pred. No. 5.9e-50;
Matches 252; Conservative 0; Mismatches 55; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 ATTCGGAA 307
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CD698821
LOCUS
DEFINITION
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AA327392.1 GI:1979637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ö
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I (bases 1 to 313)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
Mhite, O., Sutton, G., Blake, J.A., Brandon, R.C., Mann Wai, C.
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCTGCACTGGAACCAGCGATGACGTTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 CACCCAGGCAAAGCCCCCAAACTCATTATAAAGGGCTATAAACGGCCTCAGGGGTT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sess 1 to 296)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
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/tissue[rype="normal nasopharynx"
/clone lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
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Contact: Yixin Zeng
Contact: Yixin Zeng
Cancar Center
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1. .296
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                                              CD698983
CD698983.1 GI:32227826
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UI-EF-BLO-abu-b-04-0-UI.rl NIH MGC_37 Homo sapiens CDNA clone
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I (basea, 10, 323)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: ogapbs-r@mail.nih.gov
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                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 327)

Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx
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/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
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ilarity 88.5%; Pred. No. 1.5e-49;
Conservative 0; Mismatches 30; Indels C
                                                                                                                                                                                                             Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
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                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                      Email: yxzeng@gzsums.edu.cn.
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BUS84479 243 bp mRNA linear EST 20-SEP-2002
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Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
www.bio.llnl.gov/bbry/image/image.html
Seq primer: MIS Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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Incyte Genomics, Inc.
3160 Porter Drive, Palo Alto, CA 94304,
                                                                                                                                                                                           Location/Qualifiers
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1 (bases) 1 to 234)

5 Collins, J.E., Goward, M.E., Cole, C.G., Smink, L.J., Huckle, E.J., Knowless, S., Bye, J.M., Beare, D.M. and Dunham, I. Re-evaluating Human Gene Annotation: A Second Generation Analysis of Chromosome 22

1 Unpublished (2002)

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3160 Porter Drive, Palo Alto, CA 94304, USA

Tel: 650 845 4682

Fax: 650 845 5495 BUS84573 234 bp mRNA linear EST 20-SEP-2002 5559803H1 BRSTDIT01 Homo sapiens CDNA clone 5559803 5', mRNA 108 180 TGGTACCAACACCCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGG 168 61 TGGTACCAACACCACCAGGCAAAGCCCCCAAACTCATAATTTATGAGGTCACTGATCGG 120 GCCTCAGGGGTCTCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACC 228 288 9 //issue type="breast" /clone lib="BRSTDITO1" /note="breast, P? changes, mw/intraductal cancer, 48F" TCGGTCACCATCCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCC TCGATCACCATCTCCTGCACTGGAACCAGCGACGTTGGTGGTGTTATAACTATGTCTCC 121 CCCICAGGGITTCTAATCGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACC ATCTCTGGGCTCCAGGCTGAGGCTGATTATTACTGTTGTTCATACAACCAGT Gaps ó Length 243; Score 211; DB 13; Length 2: Pred. No. 2.5e-49; 0; Mismatches 20; Indels .234
 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="5559803" Tel: 650 845 4682 Fax: 650 845 5495 Email: spanzer@incyte.com. Location/Qualifiers spanzer@incyte.com. Location/Qualifiers BU584573.1 GI:23258538 63.4%; Homo sapiens (human) Query Match Best Local Similarity 91.81 Matches 223; Conservative Homo sapiens AGC 291 AGC 243 seguence. 49 н 109 169 229 241 289 source VERSION KEYWORDS SOURCE ORGANISM LOCUS RESULT 13 BU584573 REFERENCE AUTHORS ACCESSION JOURNAL FEATURES PEATURES TITLE ORIGIN ORIGIN 셤 g ò q 셤 ਨੇ ð ò ò g

BUS84480 264 bp mRNA linear EST 20-SEP-2002 4633413H1 GBLADIT02 Homo sapiens CDNA clone 4633413 5', mRNA ö 108 120 TGGTACCAACACCACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGG 168 109 169 61 GGTACCAACAGCACCAGGCAAAGCCCCCAAACTCATAATTTATGAGGTCACTGATGGGC 120 229 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[bases 1 to 264)

Collins, J. B., Goward, M.E., Cole, C.G., Smink, L.J., Huckle, E.J., Knowles, S., Bye, J.M., Beare, D.M. and Dunham, I.

Re-evaluating Human Gene Annotation; A Second Generation Analysis of Chromosome 22 121 CCTCAGGGGTTTCTAAT-GCTTCTTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCA 179 1 readreacearcrecaeredaaceaecaerearerregrecraraacrarerecre 60 9 1..264 / organism="Homo sapiens" /mol_type="mkNa" /mol_type="mkNa" /clone="4633413" /tissue_type="gallbladder" /clone_lib="GBLADITO2" /note="gallbladder, cholecystitis, cholelithiasis, 18F" 61 TGGTACCAACAACAACCCCAGGCAAAGCCCCCCAACTCATGACTTATGATGTCACTAAGGGG 121 CCTCAGGGGTCCCTGATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCCTCCCTGACC 169 GCCTCAGGGGTCTCTGATCGCTTCTGGCTCCAAGTCTGGCAACACGCGCCTCCCTGACC 1 CGATCACCATCTGCACTGGAACCAGCGACGGACGTTGGTGGTTATAACTATGTCTCCT 110 GGTACCAACACCACCCAGGCAAAACCCCCAAACTCATGATTTATGATGTCGCTAAGCGGG 50 CGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCT 170 CCTCAGGGTCTCTGATCGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCA Gabs 1; Gaps 282 181 AICTCTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCTGATCATATACA 234 229 ATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACA ö Query Match 63.0%; Score 209.8; DB 13; Length 264; Best Local Similarity 89.4%; Pred. No. 5.7e-49; Matches 237; Conservative 0; Mismatches 27; Indels 1; Length 234; Query Match
63.1%; Score 210; DB 13; Length 2
Best Local Similarity 93.6%; Pred. No. 4.7e-49;
Matches 219; Conservative 0; Mismatches 15; Indels Unpublished (2002)
Contact: Panzer SR
Incyte Genomics, Inc.
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 345 4682
Fax: 650 345 5495 49 TCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTT Bmail: spanzer@incyte.com.
Location/Qualifiers sequence. BU584480 BU584480.1 GI:23258445 Homo sapiens (human) Homo sapiens 109 source DEFINITION ORGANISM RESULT 14 BU584480 REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE JOURNAL FEATURES TITLE ORIGIN LOCUS g g ሯ ò ઠે d à 셤 ਨੇ ઠે 셤 엄 ò

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Enkaryota; Matazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 254)

NH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Exal: cgapbs-remail.nih.gov

Eco II site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Stares Lab

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.B. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: MIS Forward.
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TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGAC 227

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Search completed: June 19, 2004, 04:30:35 Job time : 1736 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic	search, using sw model	
Run on: June 1	19, 2004, 05:42:35 ; Search time 1845 Seconds (without alignments) 8833.052 Million cell updates/sec	
Title: US-09- Perfect score: 376 Sequence: 1 ggt	09-019-441A-3_COPY_48_423 6 ggtcctgtcccagctgcagctcctggtcaccgtctcctca 376	
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

., ,, ,,	Describeron	US7558 Macaca mula	AJ279514 Homo sapi	U80179 Human immun	AUZ/9520 Homo Bapı U80180 Human immun	AJ245032 Homo sapi	AJ279522 Homo sapi a.1244946 Homo sapi	AJ279549 Homo sapi	U80141 Human immun U80125 Human immun	AJ389176 Homo sapi	AY376082 Homo sapi	AJ556684 Homo sapi TR0176 Human immun	L10093 Human Ig ge	AJ245015 Homo sapi	AJZ450Z6 HOMO Bapı L10091 Human Iq qe	L12197 Human (clon	AJ245023 Homo sapi	U00532 Human immun	AJ245034 Homo sapi	AF455548 Homo sapi AT245060 Homo sapi	E12189 DNA encodin	Z46285 H.sapiens r	AJ244954 Homo sapi	AJZ44395 HOMO Sapi U00571 Human immun	U80142 Human immun	AX355946 Sequence	Mortages now sapt	AJ279527 Homo sapi	U96389 Homo sapien	AB066903 Homo sapi	AJ3UU19Z HOMO SADI AX470330 Semience	X65736 H. sapiens D	948 Homo s	AB063656 Homo sapi			linear PRI 02-OCT-1996 riable region, anti-RBC				rebrata; Euteleostomi;	; Cercopithecidae;	Cuninchem C Blancher D	· , nrament
٠	8 11)	MMUS																		3 AF455548 4 H02245060					HSUB014	AX355946	HST18012	HSA2795	HSD9638	AB066903	AX4	HSV	HSA	AB063656	ALIGNMENTS		373 bp mRNA arranged heavy chain va	,	м	(rhesus monkey)	Chordata; Craniata;	Primates; Catarrhini	מ מייילי מ יי	A.B., ADIGIGIN, S.K.,
Query	Match Length D	73.	71.4 363	71.4 363	70.1 366	69.3 363	68.4 363	68.0 363	67.9 366	67.6 375	67.3 364	67.1 363	66.9 312	66.5 354	66.1 354	65.9	65.9 375	65.5 357	65.4 360	65.4 366	65.1 372	65.1 375	65.0 360	64.9 369	64.8 365	.2 64.7 354	83 64.6 372 R 64 6 371	.6 64.5 366	42 64.4 317	42 64.4 357	4 64.3 363	.2 64.1 360	.2 64.1 363	.2 63.9 351 .2 63.9 351			stta Iq	n Ed.	31:157506	mulatta	ta	Mammalia; Butheria; Cercopithecinae: Mac	to 373)	Andris, U.S., Militar
.,	NO. SO	1 275.6																								N		1 (1)		•	N 0	1 (1)	C) (44 240		RESULT 1	LOCUS DEFINITION		VERSION	SOURCE	_		REFERENCE	

REFERENCE 1 (bases 1 to 363) AUTHORS Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F., Blancher,A. and Capra,J.D. TITLE Nariable region gene segment utilization in rheeus monkey hybridones producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34) hybridones producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34) hybridones producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34) hybridones 224966 REPERENCE ADMAISS (1997) AUTHORS Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A. and Capra,J.D. TITLE Direct Submission JOURNAL HEAVINES L. 363 1.3636.344* ADMISSION MILET MEMBAR MARKAR MILET MEMBAR MEACAGES MEMBAR MEACAGES MEMBAR MEACAGES MEMBAR MEMBA	/db_xref="G1:157506" //translation="Q000088GPGLV //translation="Q000088GPGLV GLEWIGYIYGSSGSTWNWPSLKNRVT IVPGSLDVWGRGVLVTASS" 171.8%: Score 270: D	Best Local Similarity 85.5%; Pred. No. 9.4e-65; Matches 313; Conservative 0; Mismatches 50; Indels 3; Gaps 11 CAGCTGCAGCTGCAGGACTGGAGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 11 CAGGTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCAGAGACCTGTCCCTC 11 CAGGTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCAGAGACCCTGTCCCTC	Oy 71 ACCTGGGCTGCTCTGGGGGTACTAACTGGTGGACCGGATCCGCAGGGGGGTGGATCGGCAGGATCCGCAGGGGGGGG	Qy 191 TACAACCGTCCCTCAAGAGTCGAGTCATCATTCACAAGACCGTCCAAGAACCAGTTC 250 Db 181 TACAACCGTCCCTCAAGAATCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTC 240 Qy 251 TCCTGAACCTGAACCTGTGACCGCGCGGCGTGTATTACTGTGCCAGAGAT 310 Db 241 TCCTGAAGCTGAGCTGCCGCGGGGGACACGGCGTGTATTACTGTGCCAGAGAT 310	Qy 311 FGGCCCAAATAGCTGGAACAACGCTAGGCTTCTCGGGCCAGGGACTCCTGGTCACCGTC 370 Db 301 AGCAGCTACGTTCCAGGGTCATTGGATGTCTGGGCCGGGAGTTCTGGTCACCGCC 357 Qy 371 TCCTCA 376 Db 358 TCCTCA 363	RESULT 3 HSA279514 LOCUS HSA279514 LOCUS DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone CD27low-2. ACCESSION AJ279514 VERSION AJ279514.1 GI:6723525
and Capra, J.D. Yariable Reggion Gene Segment Utilization in Rhesus Monkey Hybridomas Producing Human Red Blood Cell-Specific Antibodies: Bredominance of the VH4 Family but not VH4-21 (V4-34) Dubulished REFERENCE Andris J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D. TITLE Direct Submission JOURNAL JOURN	Query Matc Best Local Matches 3	Db 4 GGTCCTGTCCCAGGTGCAGCTGCAGGACTCGGCCCAGGACTGGTGAAGCCTTCGGAGAC 63 Qy 61 CCTGTCCCTACCTGCGCTGTCTCTGGTGACTCAGCAGTGAACTGGTGAACTGGACTGGACTG Db 64 CCTGTCCCTCACCTGCGCTGTTACTCCATCAGCAGTGGTTATAGCTGGAGTTGTAGTGGTTATAGCTGGAGTTGTAGTGGTGGTTATAGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG	Db 124 GATCGCCGCGGGGGGGGGGGGGGGTTGGGTTGGTTGTGTTGT	244 GAACCAGTTCTCCCTGAAGCTGAACTCTGTGACCGCGGGACACGGCCGTGTATTACTG 301 TGCCAGAGATTGGGCCCAAATAGCTGGAACAAGGCTAGGCTTCTGGGCCAGGGAGTCCT 101	3: SULT 2 US7559 CUS FINITION	ACCESSION US7559 MANA, partial cus. VERSION U57559.1 GI:1575065 KEYWORDS Acada mulatta (rhesus monkey) ORGANISM Macada mulatta Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

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363 bp mRNA linear PRI 01-JUN-2000 RNA for immunoglobulin mu heavy chain variable 1, clone CD2710w-2.
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85.5%; Pred. No. 9.4e-65;
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Chiorazzi,N. and Ferrarini,M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
J. Immunol. 164 (11), 5596-5604 (2000)
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Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
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                                                                                     REFERENCE
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/product="immunoglobulin heavy chain variable region"
/protein_id="AAC51094.1"
/db xref="G1:1791201"
//tb xref="G1:1791201"
/fb xref
HSUB0179 363 bp DNA linear PRI 19-FEB-1997
Human immunoglobulin heavy chain variable region (V4-4b) gene,
partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130
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1 (Dases 1 to 363)

Glas,A.M., Nottenburg,C. and Milner,E.C.
Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient
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/tissue_type="peripheral blood"
/note="CD19+ peripheral blood B cells obtained from a
healthy subject; clone 104 in reference 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 ACCTGCGCTGTCTCTGGTCGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG
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Glas,A.M., Nottenburg,C. and Milner,E.C.B.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 363
/organiam="Homo sapiens"
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/db.xref="texon:9606"
/chromosome="14"
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Gaps 9

Indels

46;

Mismatches

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317; Conservative
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/gene="IGHV4-4"
/codon start=1
/product="immunoglobulin mu heavy chain variable region"
/pro
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HORO sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone CD27low-8.
AJ279520
AJ279520.
GI:6723537
HORO CD3 I GI:6723537
HORO CD3 I GI:6723537
HORO CD3 I GI:6723537
HORO CD3 I GI:6723537
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J. Immunol. 164 (11), 5596-5604 (2000)
                              TACAACCOGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAAGTCCAAGAACCAGTTC 237
                                                                                                     TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGAGAT 310
                                                                                                                                                                                                  Direct Submission
Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
ITALY
TACAACCGTCCCTCAAGAGTCGATCATTTCACAAGACACGTCCAAGAACCAGTTC 250
                                                                                                                                      238 TCCCTGAAGCTGAGCTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGGAGAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/gene=3166
/gene=1immunoglobulin mu heavy chain variable region"
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Pred. No. 6.6e-63;
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| Organism="Homo sapiens" |
| Mol_type="mRNA" |
| Ab_zref="taxon:9606" |
| Chromosome="14" |
| Colone="CD27low-8" |
| Cell_type="IgD-low SE B-lymphocyte" |
| Fissue_type="tonsil" |
| Freagranged |
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85.9%;
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Glas, A.W., Nottemburg, C. and Milner, E.C.B.

Glas, A.W., Nottemburg, C. and Milner, E.C.B.

Direct Submission

Location/Qualifiers

Location/Qualifiers

1. .368

/ organism="Homo sapiens"

// chromosome="14"

// map="14432-433"

// clone="tt3a6"

// call type="CD19+ B cells"

// issue type="peripheral blood"

// note="CD19+ peripheral blood"

// note="CD19+ peripheral blood"

// note="CD19+ peripheral blood"

// note="CD19+ peripheral blood B cells obtained from a blood beathy subject; clone 105 in reference 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSUB0180 368 bp DNA linear PRI 19-FEB-1997 Human immunoglobulin heavy chain variable region (V4-4b) gene, partial cds.
U80180 U80180 GI:1791202
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                                                                                                                                                                                                                                                                            131 CCCCCAGGGAAGGGAACTGGAGTGGATTGGACGTACTCTCGTAGTGGGGGCCACCAAC 190
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                                                                                                                                                                                                                                                                                                                                                                                                                          178 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAAGTCCCAAGAACCAGTTC 237
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Mammalia; Butheria, Primates; Catarrhini, Hominidae; Homo.
I (bases 1 to 388)
Glas,A.M., Nottenburg,C. and Milner,E.C.
Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BWT) recipient Clin. Exp. Immunol. 107 (2), 372-380 (1997)
97182739
                                                238 TCCCTGAAGCTGAGCTCTGTGACCGCCCGGACACGCCCGTGTATTACTGTGCGAGAGAT
                                                                                                                                                               71 ACCIGCGCTGICTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG
                                                                                                                                                                                                       61 ACCIGCGCFGTCTCTCGTGGCTCCATCAGCAGTAGTAACTGGTGGAGTTGGGTCCGCCAG
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/gene="V4-4b"
/note="Ig VH4 heavy chain"
/codon_start=1</pre>
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Homo sapiens
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|||||||||||
358 GTCTCCTCA 366
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ORIGIN

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<1. .>363
/que="IGHV4-4"
/que="IGHV4-4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSA279522 363 bp mRNA linear PRI 01-JUN-2000 Homos sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone CD27low-12.
AJ279522 AJ279522. IG:6723541
IGM heavy chain; immunoglobulin mu heavy chain; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dono,M., Zupo,S., Leanza,N., Melioli,G., Fogli,M., Melagrana,A.,
Chiorazzi,N. and Ferrarini,M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
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178 TACAACCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGAACAGGTCCAAGAACCAGTTC 237
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 69.3%; Score 260.4; DB 9; Length 363; al Similarity 83.9%; Pred. No. 4.6e-62; 307; Conservative 0; Mismatches 56; Indels 3
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                                                                                                                    gene="IGHV4-4"
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Best Local S.
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AJ245032
AJ245032.1 GI:4995522
AJ245032.1 GI:4995522
FMI 1gM heavy chain; immunoglobulin mu heavy chain, variable region.
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Chiorazzi,N. and Ferrarini,M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalence
J. Immunol. 164 (11), 5596-5604 (2000)
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121 CCCCCAGGGAAGGGCTGGAGTGGATTGGGGAATCTATCATA---GTGGGAGCACCAAC 177
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Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
                                                                                                                                                                                                                                                                             9
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                 CAGGTGCAGGAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGGGACCCTGCCTC
                                                                                                                                                                                                                                                                                                                                                 71 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGAGCCTGGATCCGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACAACCCGTCCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                            11 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                    8;
                                                                                                                                                            Length 368;
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                                                                                                                                                         Query Match 69.9%; Score 263; DB 9;
Best Local Similarity 85.7%; Pred. No. 8.6e-63;
Matches 318; Conservative 0; Mismatches 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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297

9

3; Gaps

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                                                                          Dono,M.
Direct Submission
Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova, ITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 ACCIGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGGGACCTGGATCCGCCAG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAACTGGTGGAGTTGGGTCCGCCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCCCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGTGGGCCACCAAC 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.4%; Score 257.2; DB 9; Length 363; Similarity 83.3%; Pred. No. 3.6e-61; 5; Conservative 0; Mismatches 58; Indels 3
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J. Immunol. 164 (11), 5596-5604 (2000)
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                                                            (bases 1 to 363)
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Dono,M., Zupo,S., Leanza,N., Melioli,G., Fogli,M., Melagrana,A., Chiorazzi,N. and Ferrarini,M. Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

IgM; IgM heavy chain; immunoglobulin mu heavy chain; variable

partial, clone 3-A1

AJ244946 AJ244946.1 GI:4995351

ACCESSION VERSION KEYWORDS

7.00

Homo sapiens (human) Homo sapiens

ORGANISM

SOURCE

AUTHORS REFERENCE

TITLE

region

Ricerca

Istituto Nazionale per la Rice. L.go Rosanna benzi 10- Genova,

Direct Submission Submitted (24-MAY-1999) Dono M., sul Cancro, Immunologia Clinica, ITALY

TITLE JOURNAL

source

FEATURES

10820234 2 (bases 1 to 363) Dono, M.

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                <li..>>363
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HSA244946 363 bp mRNA linear PRI 01-JUN-2000 Homo sapiens mRNA for immunoglobulin mu heavy chain variable

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                                                                                                                                                                                                  191 TACAACCGTCCCTCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTC 250
178 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGAACAAGTCCAAGAACCAGTTC 237
                                                                                                                                                                                                                                                                                                                                     61 ACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAACTGGTGGAGTTGGGTCCGCCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 AGCGTAGGTCTACCCTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTC 357
                                                                                                          .>366
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Homo sapiens
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HSU80141
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Dono,M., Zupo,S., Leanza,N., Melioli,G., Fogli,M., Melagrana,A.,
Chiorazzi,N. and Ferrarini,M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
0. Immunol. 164 (11), 5596-5604 (2000)
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                                311 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGGGTCTGGTCACCGTC 370
298 GAGTGGTTAGGCGCCTTGTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
ITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTCCCCTCTCTCTCTCTCTCTCACCAGTACTACTCGTGGACCTGGATCCGCCAG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGGIGCAGCIGCAGGAGIGGGCCCAGGACIGGAAGCCIICGGGGACCIIGICCCCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU279569.1 GI:6723593
immunoglobulin heavy chain; variable region; VH4 family.
Homo sapiens (human)
Homo sapiens sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                            371 TCCTCA 376
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<1. .327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGVH gene), sample GN08.
                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (20-UUL-1999) Fais F., Clinical Immunology, Istituto
Submitted Per la Ricerca sul Cancro, L.go R. Benzi 1, 16132, ITALY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  121 CCCCCAGGGAAGGGGCTGGAGATTGGGGAAATCTATCATA---GTGGGAGCACCAAC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 TCCCTGAAGCTGAGCTCTGTGACGCCGCGGGACGTGTGTTACTGTGCGAAATCCC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 TACAACCGTCCCTCAAGAGTCGACATCATTTCACAAGACAGTTC
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IGVH gene; immunoglobulin heavy chain; variable region.
Homo sapiens
Homo sapiens
                                                                                                                                                                                                         Length 364;
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358 CTCCTCA 364
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/clone="3g499"
/cell_type="CD19+ B ceils"
/cell_type="CD19+ B ceils"
/tissue_type="peripheral blood"
/note="CD19+ peripheral blood B cells obtained from a bone marrow transplant recipient 90 days post transplant; clone 50 in reference 1"
/gene="V4-4b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nsuguzzs 364 bp DNA linear PRI 19-FEB-1997
Human immunoglobulin heavy chain variable region (V4-4b) gene,
partial cds.
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Glas.A.M., Nottenburg,C. and Milner,E.C.B.
Glas.A.M., Nottenburg,C. and Milner,E.C.B.
Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, RA 98101, USA
Location/Qualifiers
                                                                                                                                                         311 TGGGCCCAAATAGCTGGAA---CAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC 367
298 CCCGCAGTGGTACGACCCCTATCTTTGACTACTGGGGCAACCCTGGTCACC 357
                                                                                                                                                                                                                                 190
                                                                                                                                                                                                                                                                                                 250
                                                                                                                                                                                                                                                                                                                                  237
                                                                                                                                                                                                                                                 TCCCTGAACCTGAACTCTGTGACCGCGGGACACGGCCGTGTATTACTGTGCCAGAGAT 310
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1 (bases 1 to 34).

1 (bases 1 to 34).

1 (bases 1 to 34).

1 Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient Clin. Exp. Immunol. 107 (2), 372-380 (1997)
                                                                                                                                                                                                                                                                                                                                                                                        238 TCCCTGAAGCTGAGCTCTGTGAGCTCGCGGGACACGCCGTGTATTACTGTGCGAGAGTC
                                                                                                           1 CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGGGACCCTGTCCCTC
                                                                                                                                                                                                                                                                                                                    178 TACAACCGSTCCCTCAAGAGTCGACCACCATATCAGTAGACAAGACCAGTTC
                                                                                                                                                                                                                                 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAAC
                                                                                                                                                                                                                                                                                                   TACAACCOGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                        11 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGATGAAGCCTTCGGAGACCCTGTCCCTC
                                                         Gaps
                                                         9
                       Length 366;
                    Score 255.4; DB 9; Length
Pred. No. 1.2e-60;
0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="14"
                      tch 67.9%;
al Similarity 84.6%;
312; Conservative
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U80125.1 GI:1791092
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                    Query Match
Best Local S:
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PRI 02-JUN-2003
heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGCCCACCAACT 191
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AJ556684 GI:31337609 IGHV4-04 gene; immunoglobulin gamma heavy chain; variable region. IGHV4-04 gene; immunoglobulin gamma heavy chain; variable region. Homo sapiens (human) Homo sapiens (buman) Homo sapiens (human) Homo sapiens (hu
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Maintenance of B lymphocytes related clones in the cerebrospinal fluid of multiple sclerosis patients
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGGTGCAGCTGCTCGAGTCGGGCCCAGGACTGGTGAGCCTTCGGAGACCCTGTCCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 CCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGAGCTGGATCCGCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 ACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACCACGAAGAACCAGTTCT
                                                                                                                                                                                                                                    <1. .>364
/note="VH domain; VH-D-JH segments of amplified VH-CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.3%; Score 253; DB 9; Length 36 larity 82.7%; Pred. No. 5.4e-60; Conservative 0; Mismatches 60; Indels
                         Location/Qualifiers
1. 364
Acganism="Homo aspiens"
/mol type="mRNA"
/isolate="VH-CB-A54"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                     transcript; Ig"
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Colombo, M.
Direct Submission
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1 (Dases I to 364)
Davies, J.M. and O'Hehir, R.E.
WH gene usage in IgE responses of grass pollen allergic individuals is oligoclonal and antigen driven
                                                                                                                                                                                                                          /goncinosimume response"
/codon start=1
/codon start=1
/poduct=rimmunoglobulin heavy chain variable region"
/protein_id="CAB51716.1"
/db_xref="G1:5679482"
/db_xref="G1:567948"
/db_xref="G1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ACCTGCACTGTTCTTGTTACTCCATCAGCAGTTACTACTAGGGGTTGGATCCGGCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CCCCCAGGGAAGGGGCTGGATTGGGAGTATCTATCATA---GTGGGAGCACCTAC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 TGGGCCCAAATAGCTGGAACAACGCTTGGGGCCCAGGGAGTCCTGGTCACCGTC 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 TGGATACAGCTA---TGGTCAGACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC 354
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2 (Dases 1 to 364)

Davies, J.M. and O'Hehir, R.E.

Direct Submission

Submitted (28-AUG-2003) Allergy, Immunology and Respiratory
Medicine, The Alfred Hospital, Commercial Road, Melbourne, VIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 TACAACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGAACGACGTCCAAGAACCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 254; DB 9; Length 375;
Pred. No. 2.8e-60;
0; Mismatches 50; Indels
cell_type="B-lymphocyte"
rearranged
                                                            /note="sample GN08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY376082.1 GI:37014228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.7%;
Matches 310; Conservative (
                                                                                                                                                                    :1. .>375
/gene="IGVH"
                                                                                                                                    "gene="IGVH"
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Homo sapiens
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TCCTCA 360
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/procein_id="CAD89411.1"
/db_xref="G1:3137610"
/fb_translation="QLOLOESGPGLVKPSGTLSLTCAVSGGSVSSGDWWTLVRQPPGK
GLEWIGELYHSGSTRYNPSLASRATISVDKSKNQFSLMLSSVTAADTAVYYCTRWSFY
DRGGVFDIWGGGTMVTVSS"
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Submitted (26-FEB-2003) Colombo M., Medical Oncology C, IST-Ist. Nazion. Ricerca Cancro, Lrgo Rosanna Benzi 10, Genova 16132, ITALY Location/Qualifiers
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/gene="IGHV3-07"
/product="immunoglobulin gamma heavy chain variable
region"
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/gene="IGHV4-04"
/gene="IGHV4-04"
/codon glart=1
/product="immunoglobulin gamma heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 67.1%; Score 252.4; DB 9; Length 363; Best Local Similarity 82.5%; Pred. No. 8e-60; Matches 302; Conservative 0; Mismatches 61; Indels 3
                                                                                                       | ...363 | // organism="Homo sapiens" | // organism="Homo sapiens" | // organism="Homo sapiens" | // organism="Homo sapiens" | // organism="14" | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .363
/gene="IGHV3-07"
1. .363
/gene="IGHV4-04"
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Search completed: June 19, 2004, 07:02:22 Job time : 1848 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	ncleic - nucleic search, using sw model	on: June 19, 2004, 05:41:30 ; Search time 276 Seconds (without alignments) 5787.400 Million cell updates/sec	set score: 376 ince: 1 ggtectgteccagetgcagetectggteacegtetectea 376	ng table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	hed: 3373863 segs, 2124099041 residues	Total number of hits satisfying chosen parameters: 4296338	num DB seq length: 0 num DB seq length: 376	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Asse : N_Geneseq_29Jan04;* 1: geneseqn1980s:* 2: geneseqn1990s:* 3: geneseqn2000s:* 5: geneseqn2001as:* 6: geneseqn2001as:* 7: geneseqn2003as:* 8: geneseqn2003cs:* 10: geneseqn2003cs:*
	OM nucleic -	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number	Minimum DB s Maximum DB s	Post-process	Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Abk24412 Heavy cha	Aat45035 Human lun	Abs57441 Human mon	Aba94218 ebvHigM M	Abs62713 Germline	Aax25318 Multiple	Abs62723 Anti-IGF-	Abs20941 Human gen	Ade28490 Human ant	Aaq33035 MAb 1-3-1	Aaz49608 DNA-1 rel	Aaz49590 Human ant	Aak20407 Human bra	Ade28446 Human ant	Ade28454 Human ant	Aas03440 DNA encod	Aaf29046 Human HIV	Aaf29051 Human HIV	Aaq42697 Vh 71-4.	Aaq42700 VH415. 3/	Aaq42699 VH411. 3/	Ade28414 Human ant	Aaf29059 Human HIV
SUMMARIES	ABK24412	AAT45035	ABS57441	ABA94218	ABS62713	AAX25318	ABS62723	ABS20941	ADE28490	AAQ33035	AAZ49608	AAZ49590	AAK20407	ADE28446	ADE28454	AAS03440	AAF29046	AAF29051	AAQ42697	AAQ42700	AAQ42699	ADE28414	AAF29059
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% Query Match Length	354	372	360	363	296	294	358	362	364	366	351	351	319	364	364	351	369	372	348	348	348	357	360
% Query Match	64.7	64.6	64.6		64.2	64.1	62.6	62.6	62.4	62.4	62.3	62.3	62.2	62.0	62.0		61.8	61.8	61.6	61.6	٠	61.6	61.4
Score	243.2	243	242.8	242.8	241.4	241	235.4	235.2	234.6	234.6	234.4	m	233.8	233	233	232.4	232.4	232.2	231.8	231.8	37	231.6	231
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Aag42701 VH416. 3/	Abs68607 DNA encod	Ade28422 Human ant	Aaf29506 Human Fab	Ada89273 Human ant	Abs62718 Germline	Abs62725 Anti-IGF-	Aax25317 Multiple	Abs62714 Germline	Aag42702 Ab26. 3/2	Ada89257 Human ant	Aaf29066 Human HIV	Adc99798 Anti-huma	Add05402 Anti-MUC1	Aaf29076 Human HIV	Adc99782 Anti-huma	Adc99810 Anti-huma	Add05414 Anti-MUC1	Add05386 Anti-MUC1	Aas03454 DNA encod	Abs46332 Human liv	Aaq42698 F105Vh. 3
AAQ42701	ABS68607	ADE28422	AAF29506	ADA89273	ABS62718	ABS62725	AAX25317	ABS62714	AAQ42702	ADA89257	AAF29066	ADC99798	ADD05402	AAF29076	ADC99782	ADC99810	ADD05414	ADD05386	AAS03454	ABS46332	AAQ42698
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61.2	60.7	60.7	60.2	60.1	59.9	59.9	59.8	59.5	59.5	59.4	59.3	59.2	59.2	59.0	59.0	59.0	59.0	59.0	58.8	58.7	58.7
230.2	228.2	228.2	226.2	225.8	225.4	225.4	224.8	223.8	223.8	223.2	222.8	222.6	222.6	222	221.8	221.8	221.8	221.8	221.2	220.8	220.6
24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 .5

ALIGNMENTS

BP.

ABK24412 standard; DNA; 354

ABK24412;

Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody; prikA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy; peripheral neuropathy; dabetic neuropathy; neurodegenerative disease; large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour; nerve cell injury; blood cell disorder; leukopaenia; cancer; wound; basopaenia; lymphopaenia; monocytopaenia; neuropaenia; cancer; alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes; sickle cell disease; cardiac ischaemia; cerebrovascular disorder; cellular degeneration; gene therapy; ds; gene. Heavy chain DNA from human anti-trkC agonist monoclonal antibody #4. Devaux B, Hongo JS, Presta LG, Shelton DL; 22-JUN-2000; 2000US-0213141P. 05-0CT-2000; 2000US-0238319P. 22-JUN-2001; 2001WO-US020153 09-APR-2002 (first entry) (GETH) GENENTECH INC WO200198361-A2. Homo sapiens. 27-DEC-2001. RESULT 1
ABK24412
XX
ACC ABK2.
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CELLIA
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CELLIA

WPI; 2002-130790/17. P-PSDB; AAU81276.

Novel anti-trkC agonist monoclonal antibody useful for treating neurodegenerative disease, shows no significant cross-reactivity with trkA/trkB, and recognizes epitope in domain 5 of trkC.

Claim 38; Fig 28; 121pp; English.

The invention relates to an anti-trkC agonist monoclonal antibody which shows no significant cross-reactivity with trkA or trkB, and recognizes

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29-OCT-1996
      misc_RNA
                                                       misc_RNA
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                                                                                                                                                                                                                                                                                                                                   ACCIGCACIGICACTGGGGGCTC---CAICAGTACTTACTGACTGGAACTGGCAG 117
                                                                                                                                                                                                                                                                                                                                                                    CCCCCAGGGAAGGGACTGGACTGGACGTATCTCTGGTAGTGGTGGCGCCCACCAAC 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGCCCAAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACGGCC 370
an epitope in domain 5 of trKC. The antibodies of the invention are effective in the treatment of cisplatin- or pyridoxine-induced neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre sensory neuropathy, neurodegenerative disease including amyotrophic lateral sclerosis, nerve cell injuries, disorders of insufficient blood cells such as leukopaenia including eosinopaenia, basopaenia, lymphopaenia, monocytopaenia, neuropaenia, Alzheiner's disease, lymphopaenia, monocytopaenia, neuropaenia, Alzheiner's disease, lorkinson's disease, Huntington's disease and tumours. The sequences also useful for inducing angiogenesis for treating wounds, ulcers and diabetic complications of sickle cell disease, for treating cardiac ischaemia and cerebrovascular disorders and in the diagnosis of diseases involving cellular degeneration. Sequences ARK24399-ABKA4413 represent antibodies and antibody fragments of the invention
                                                                                                                                                                                                                                                                                                                     ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 130
                                                                                                                                                                                                                                                                                                                                                                                    CCCCCCGGGAAGGGACTGGAGTGGATTGGGCGTATCT---ATACCAGTGGGACCAAC 174
                                                                                                                                                                                                                                                                                1 CAGGTGCAGCTGCAGGTGTGGGCCCCAGGACTGGTGAGGCCTTCGGAGACCCTGTCCCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy chain; light chain; variable region; human; monoclonal antibody; lung cancer tissue; diagnosis; purification; cancer-specific antigen; ss.
                                                                                                                                                                                                                                                                  11 CAGCTGCAGCTGCAGGAGTCGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                                                                                                                                                               Query Match 64.7%; Score 243.2; DB 6; Length 354;
Best Local Similarity 85.0%; Pred. No. 1.6e-57;
Matches 311; Conservative 0; Mismatches 43; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lung cancer specific antibody heavy chain variable region cDNA
                                                                                                                                                                                          Sequence 354 BP; 73 A; 107 C; 103 G; 71 T; 0 U; 0 Other;
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/*teg= a
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/note= "Fig 5, Claim 7
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TCCTCA 354
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misc_RNA
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 AATTACGATTTTTGGAGTGGTGGCGACGGGCCATTTGACTACTGGGGCCAGGGAACGCTG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAT45035-36 encode the heavy chain and light variable regions from a human monoclonal antibody which is specific human lung cancer tissue. The encoclonal antibody may be used for clinical diagnosis of cancers, for immunological therapy or for purification of a cancer-specific antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 372 BP; 77 A; 102 C; 117 G; 76 T; 0 U; 0 Other;
151. .198
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295. .339
                                                                                                                                                      Claim 7"
                                                                                                                                   "CDR3"
                                                                                                                                   /product= "CDR3
/note= "Fig 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
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                                                                                                                                                                                                                                                                                            95JP-00112671
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P-PSDB; AAW06474.
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Human; monoclonal antibody; Fl.1; Mab Fl.1; heavy chain variable region; gene; ss; antigen-binding protein; alpha3(lV) NCI collagen; anti-GBM disease; anti-glomerular basement membrane autoantibody disease; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                  New human monoclonal antibody or its antigen-binding protein that specifically binds alpha 3(IV) NCI collagen, useful for preparing compositions for treating or preventing anti-glomerular basement membrane disease.
                                                                                                                                         1. .360
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/product= "Human Mab F1.1 heavy chain variable region"
                                      Human monoclonal antibody Fl.1 heavy chain variable region cDNA
                                                                                                                                                                      /partial
/note= "No start or stop codon shown"
                                                                                                                               location/Qualifiers
                                                                                                                                                                                                                                             23-APR-2002; 2002WO-US013063.
                                                                                                                                                                                                                                                                23-APR-2001; 2001US-0285860P
                   (first entry)
                                                                                                                                                                                                                                                                                    (ABGE-) ABGENIX INC.
(UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                  Gallo ML;
                                                                                                                                                                                                                                                                                                                                     WPI; 2003-093089/08.
P-PSDB; ABG71454.
                                                                                                                                                                                                      WO200285924-A2
                                                                                                             Homo sapiens
                  20-FEB-2003
                                                                                                                                                                                                                         31-OCT-2002
                                                                                                                                                                                                                                                                                                                  Madaio MP,
ABS57441;
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The invention relates to a human monoclonal antibody or its antigen-binding protein which specifically binds alpha1(IV) NCI collagen and a hybridoma cell line that produces the F1.1 monoclonal antibody. The human monoclonal antibody or its antigen-binding protein that specifically binds alpha1(IV) NCI collagen is useful for preparing compositions for treating or preventing human anti-glomerular basement membrane autoantibody disease (anti-GBM disease). The sequences can also be used for producing a mouse model for anti-GBM disease, for inducing anti-GBM disease in a mouse and for screening or identifying compositions for treating or preventing one or more symptoms of anti-GBM disease. This sequence represents obNA encoding a human monoclonal antibody F1.1 (Mab F1.1) heavy chain variable region. Claim 13; Page 61; 80pp; English.

Sequence 360 BP; 73 A; 110 C; 101 G; 76 T; 0 U; 0 Other;

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130
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                                                                                                                                                                                                                                131 CCCCCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 190
                                                                                                               1 CAGGIGCAGCIGCTCGAGICGGGCCCAGGACTGGIGAAGCCTTCGGGGACCCTGTCTCTC 60
                                                                                                                                                        71 ACCTGCGCTGTCTCTGGTCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG
                                                                                                                                                                              61 ACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTACTAACTGGTGGACTTGGGTCCGCCAG
                                                                                                                                                                                                                                                      TCCCCAGGAACGGACTGGACATATCTATCATA---GTGGGAGCACCCCCAC
                                                                            11 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCCTTCGGAGACCCTGTCCCTC
                                         9
64.6%; Score 242.8; DB 7; Length 360; 82.8%; Pred. No. 2.1e-57; Indels 6.
                  Local Similarity ....
Query Match
                        Best Loca
Matches
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The invention provides a neuromodulatory agent (I) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CMS). (I) is capable of inducing remyelination, promoting callular proliferation of glial cells, and promoting Ca2+ signaling with oligodenfrocytes. An humanised antibody to (I) can be selected from antibody sHIGMS2 (LMM 22), ebvHigM MSIJBIO, ebv HIGM CB2bG8, AKMR4, CB2iBI2, CB2iET or MSIJBES. (I) is useful for stimulating remyelination of CNS axons, or treating demyelinating proliferation of glial cells in CMS axons, or treating demyelinating disease of CNS in a mammal in need of such therapy. (I) is capable of blinding to structures and cells within CNS. (I) is preferably useful for treating a demyelinating disease of CNS of a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TMEW) or for treating a human being having multiple sclerosis, or a

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250
                    237
                                           251 TCCCTGAACCTGAACTCTGTGACCGCGGGGACACGGCCGTGTATTACTGTGCCAGAGAT 310
                                                                294
                                                                                     311 TGGGCCCAAATAGCTGCAACAACGCTAGGCTTCTGGGGCCAGGGGAGTCCTGGTCACCGTC 370
295 GCGGCCCAGTATCACTGGAAGGGGTTCGACCCCTGGGCCCATGGAACCCTGGTCACCGTC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis.
191 TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCCAAGAACCAGTTC
           178 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAATAGACAGTCCAAGAATCAATTC
                                                        Neuromodulatory, central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHigM MsI19D10; ebv HIGM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerary; ds.
                                                                                                                                                                                                                                                                               ebvHigM MSI19D10 heavy chain variable region nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAYO-) MAYO FOUND MEDICAL EDUCATION
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 43; Fig 19; 219pp; English.
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                                                                                                                                                                                                              ABA94218 standard; DNA; 363 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000; 2000WO-US014902
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                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodriguez M, Miller DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-066596/09.
P-PSDB; ABB07171.
                                                                                                                                              355 TCCTCA 360
                                                                                                                                  TCCTCA 376
                                                                                                                                                                                                                                                                                                                                                                                                                  W0200185797-A1
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(PFIZ) PFIZER INC. (ABGE-) ABGENIX INC.

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human or domestic animal with a viral demyelinating disease, or a postneural disease of CNS. (1) is also useful for an in vitro method of stimulating the proliferation of glial calls from mixed cell culture. (1) is also useful for stimulating remyelination of CNS axons. The antibodies are useful for preventing infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition in a subject. Methods where (1) is administered to a patient are useful for treating multiple sclerosis, Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating disease, CNS diseases, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents the ebvHigh MSI19910 heavy chain variable region nucleotide sequence
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Sequence 363 BP; 77 A; 106 C; 105 G; 75 T; 0 U; 0 Other;

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CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 190
                                                                                                                                                                   TACAACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTC 250
                                                                                                                                    CCCCCAGGAAAGGACTGGAGTGGGTATACTATACA---GTGGGAGCACCAAC 174
                                                                                                                                                                                TOCCTGAACCTGAACTCTGTGACCGCGGGGACACGGCCGTGTATTACTGTGCCAGAGAT 310
                                                                                                                                                                                                                     1 CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTC 60
                                         CAGCTGCAGCAGCAGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC
                       9
  64.6%; Score 242.8; DB 6; Length 363; larity 82.8%; Pred. No. 2.1e-57; Conservative 0; Mismatches 57; Indels 6;
Query Match
Best Local Similarity
Matches 303; Conserva
                                                                                                                                                                                                                                                                                                     TCCTCA 360
                                                                                                                                                                                                                                                                                            TCCTCA 376
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Insulin-like growth factor I receptor; antibody; human; ds; gene; cytostatic; osteopathic; antibatherosclerotic; antiposriatic; IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-anglogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis; atherosclerosis Sermline anti-IGF-1R antibody (VH-DP-70) heavy chain DNA 쁌. ABS62713 standard; DNA; 296 (first entry) 24-OCT-2002 ABS62713

W0200253596-A2, Homo sapiens

20-DEC-2001; 2001WO-US051113

05-JAN-2001; 2001US-0259927P

This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to contibody or its antigen binding portion that specifically binds to contibody or its antigen binding of IGP-IR. The antibodies of the invention can act as an inhibitor of binding of IGP-I or IGP-II with IGP-IR phosphorylation. The antibodies of the invention are useful for the antibody or its antigen-binding portion is also useful for chargener in a human. The method for this further involves an antice complexit, anti-tumour, anti-angiogenic or chemotherapeutic agent. The antibodies may also be useful for increasing IGP-IR activity and thus continuous in IR activity and condition characterised by low IGP-IR cereivity in a condition characterised by low IGP-IR cereivity in a condition characterised by low IGP-IR activity in a condition characterised by Iow IGP-IR cereivity in a condition characterised by Iow IGP-IR also useful for inducing apoptosis of specific cells in a patient, and to creat non-canecrous states or disease, e.g. acromegaly, gigantism, concanecrous states or disease, e.g. acromegaly, gigantism, concanecrous states or disease, e.g. acromegaly, gigantism, or concansis and atherosclerosis Pully human anti-IGP-IR antibodies or mouse-derivatised monoclonal antibodies and thus increase the efficacy and safety of the administered antibodies. The present sequence receptor antibody of the invention Novel humanized, chimeric monoclonal antibody that specifically binds to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in humans. Σ Gallo Corvalan JR, Moyer JD, Disclosure; Page 137; 172pp; English. Miller PB, Cohen BD, Beebe J, 2002-575410/61 P-PSDB; ABG77151

Sequence 296 BP; 64 A; 83 C; 92 G; 57 T; 0 U; 0 Other;

71 ACCIGCGCTGTCTCTGGTGGCTCTCTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 130 61 ACCTGCGCTGTCTTGGTGGCTCCATCAGCAGTAGTAACTGGTGGAGTTGGGTCCGCCAG 120 190 237 191 TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 250 9 20 178 TACAACCGGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAAGTCCAAGAACCAGTTC CCCCCAGGGAAGGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGGCCACCAAC 3; Gaps Query Match 64.2%; Score 241.4; DB 6; Length 296; Best Local Similarity 90.3%; Pred. No. 4.8e-57; Matches 270; Conservative 0; Mismatches 26; Indels 3; 131 셤 ద જે 쉽 ద ઠે 셤 ઠે

AAX25318 standard; DNA; 294 RESULT 6
AAX25318
XD AAX21
XX AC AAX2
XX DT 19-JU
XX DE MULT:
XX

19-JUL-1999 AAX25318;

(first entry)

Multiple sclerosis patient CSF B-cell VH gene clone 4d68

Multiple sclerosis, cerebrospinal fluid; CSF; B-cell, heavy chain variable region; VM gene; somatic hypermutation; B-cell clonality; ML gene; diagnosis; human; ss.

Determination of B-cell clonality by amplification or enzymatic

*PI; 1999-276985/23. P-PSDB; AAY05693

NIO (/ANIO)

Qin Y;

replace [163,G]
/*tag= e
/note= "mutation in CDR2 compared with ML" replace (170,C)
/*tag= f
/note= "mutation in CDR2 compared with ML" /*tag= g /note= "mutation in CDR2 compared with ML" replace(177,G) /*tag= i /note= "mutation in CDR2 compared with ML" replace(185,T) /note= "mutation in CDR2 compared with ML" replace (183,T) /*tag= d /note= "mutation in FR1 compared with ML" /note= "mutation in FR1 compared with ML' compared with ML' /note= "mutation in FR1 compared with ML" /*tag= r /note= "mutation in FR3 compared with ML" /*tag= j /note= "mutation in FR3 compared with ML" compared with ML' /*tag= 1 /note= "mutation in FR3 compared with ML" replace(234,T) /*tag= m /note= "mutation in FR3 compared with ML' /*tag= n /note= "mutation in FR3 compared with ML' replace(251,A) /*tag= o /note= "mutation in PR3 compared with ML" 'note= "mutation in FR3 compared with ML" compared with ML' /uransl except= (pos:16. .18, aa:Gly)
replace[15,A)
/*tag= b replace (19,T)
/*tag= a
/note= "mutation in FR1 /*tag= k /note= "mutation in FR3 in FR3 ocation/Qualifiers /*tag= p /note= "mutation replace(284,T) replace(176,G) /*tag= g replace (221,G) replace (214, A) replace (232, A) replace (249,C) replace (252,G) replace (78, A) replace(75,G) /*tag= c *tag= Homo sapiens WO9915696-A1 01-APR-1999 mutation

This is the nucleotide sequence of the heavy chain variable region (VH)

gene from a dominant clone, termed 4d68, of B-cells taken from the

cerebrospinal fluid (CSF) of a multiple sciencis (WB) patient. Sequences

of VH of CSF B-cells were obtained from 4 MS patients (see AAX25316-19).

Differences in nucleotide and predicted amino acid (see AAY05691-94)

Sequences were compared with the closest known germline VH genes; for
4d68, this was ML. The results provided direct vidence that intrathecal

clonally expanded B-cells from the CSF of MS patients are hypermutated

postgerminal centre antibody-forming or memory lymphocytes that havd

undergone antigen selection. This finding implicates an important

pathogenic pathway for the development of demyelination in CNS of MS. The

invention provides assay kits for determining B-cell or T-cell clonality.

This technology allows the establishment of clonal specific RNA library

from pathogenic cells in the CNS of patients, which is important for

curcher understanding of the role of antigen specific therapeutic

clonal expansion, and towards developing antigen specific therapeutic 71 ACCTGCGCTGTCTCTGGGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 130 61 ACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTAGTAACTGGTGGAGTTGGGTCGCCCAG 120 131 CCCCCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 190 121 CCCCCAGGGAAGGGCTGGAGTGGGAAATCTATCATA---GTGGGAGCACCAAC 177 191 TACAACCOGTCCCTCAAGAGTOGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 250 2 9 11 CAGCTGCAGCTGCAGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC Gaps Score 241; DB 2; Length 294; Pred. No. 6.2e-57; 0; Mismatches 25; Indels Sequence 294 BP; 62 A; 84 C; 91 G; 57 T; 0 U; 0 Other; Disclosure; Fig 9B; 67pp; English. ABS62723 standard; DNA; 358 BP. Match 64.1%; Local Similarity 90.6%; Hes 269; Conservative 24-OCT-2002 (first entry) Query Match ABS62723; Best Loca. Matches RESULT 7 ABS62723 ð d ò 셤 셤 요 ò 8 8

Insulin-like growth factor I receptor; antibody; human; ds; gene; cytostatic; osteopathic; antiatherosclarotic; antipsoriatic; IGF-IR; tumour; anti-neoplastic; anti-tumour; anti-anglogenic; neuropathy; osteoporosis; acromegaly; gigantism; psoriasis; atherosclerosis.

97CA-02216595. 97CA-02220245.

19-SEP-1997; 04-NOV-1997;

Anti-IGF-IR antibody VH chain DNA consensus sequence #2.

This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulini-like growth factor I receptor (167-18). The antibodies of the invention can act as an inhibitor of binding of 16F-IR tyrosine.

IR and can inhibit in vivo tumour growth and IGF-IR tyrosine of phosphorylation. The antibodies of the invention are useful for diagnosing the presence or location of an IGF-IR expressing tumour in a subject. The antibody or its antigen-binding portion is also useful for treating cancer in a human. The method for this further involves an antipodoies may also be useful for increasing IGF-IR activity in a condition characterised by low IGF-IR restoring IGF-IR activity in a condition characterised by low IGF-IR levels e.g. neuropathy, or osteoporosis. An antibody of the invention is also useful for inducing apoptosis of specific cells in a patient, and to treat non-cancerous states or disease, e.g. acromegaly, gigantism, psoriasis and atherosclerosis. Pully human anti-IGF-IR antibodies minimise the immunogenic and allergic responses intrinsic to mouse or mouse-derivatised monoclonal antibodies and thus increase the efficacy and safety of the administered antibodies. The present sequence repersents a DNA sequence encoding an anti-insulin-like growth factor I creceptor antibody of the invention Novel humanized, chimeric monoclonal antibody that specifically binds to insulin-like growth factor I (IGF-1) receptor useful for inhibiting binding of IGF-I or IGF-II to receptor and for treating cancer in humans. Σ, Gallo Corvalan JR, Moyer JD, Disclosure; Fig 23; 172pp; English. Miller PE, 20-DEC-2001; 2001WO-US051113. 05-JAN-2001, 2001US-0259927P. Beebe J, (PFIZ) PFIZER INC. (ABGE-) ABGENIX INC. WPI; 2002-575410/61 WO200253596-A2 Homo sapiens. 11-JUL-2002 Cohen BD,

Sequence 358 BP; 70 A; 103 C; 101 G; 79 T; 0 U; 5 Other;

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ACCTGCACTGTCTCTGGTGGCTC---CATCAGTARTTACTACTGGAGCTGGATCCGGCAG 117 TACAACCOSTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTC 250 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 130 CCCCCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGCCCACCAAC 190 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 310 311 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGGCCCAGGGAGTCCTGGTCACCGTC 370 235 TCCCTGAAGCTGARCTCTGTGACCGCGGGGACACGGCCGTGTATTACTGTGC---GGTA 291 11 CAGCTGCAGCTGCAGAGTCGCGCCAGAGTGAGCCTTCGGAGACCCTGTCC 70 1 CAGGIGCAGCIGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTC 60 Gaps . . Query Match 62.6%; Score 235.4; DB 6; Length 358; Best Local Similarity 82.5%; Pred. No. 2.3e-55; Matches 302; Conservative 4; Mismatches 51; Indels 9; 71 61 131 118 191 175 251

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from the human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 to probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which Mybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the agorithmically predicting at least one exon from genomic sequences of the array; identifying exons in a ewaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the ewing a fragment identical to the predicted exon, the probe is included thaving a fragment identical to the predicted exon, the probe is included the above mentioned microarray; assigning exons the probe is included comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of the exons in several
                                                                                                                                                                                                                                                                                       Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous solerosis; gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicytosis; lymphangioleiomyomcosis; Karagemer syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary hypertension; primary cillary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                                                                                                              Human genome-derived single exon probe ORF from lung SEQ ID No 20932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; SEQ ID NO 20932; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-02707456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00533565.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-02359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000665
                                                                                                                ABS20941 standard; DNA; 362
                                                                                                                                                                                                   19-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-114183/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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  352
                                                                                                                                                           ABS20941;
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292 ACGAITITIGGAGIGGITATIAICITIGACTACTGGGGCCAGRGANCCCTGGICACCGTC 351

371 TCCTCA 376

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tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the expression of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the composition of the stands (DRF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human analysis, and for identifying exons in a gene, particularly using human concern, chronic obstructive pulmonary fluoresesses such as asthma, lung cancer, chronic obstructive pulmonary fluoreses (CDPP), interstitial lung disease (LLD), familial idiopathic pulmonary fluoresis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-cholars, rymdrome, sarcoidosis, pulmonary alveolar proteinosis, histocytosis, lymphangioleiomyconicosis, pulmonary alveolar proteinosis, Kazagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the present exception, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pot_sequences
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Sequence 362 BP; 79 A; 103 C; 109 G; 71 T; 0 U; 0 Other;

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                                                                                                                                                                                 118 CTGGATCCGCCAGGCACAGGAAGGAACTGGAATGGACTGGACTGGATTGGACTTGTATTCTCTGGTAGTGG 177
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                                                                                                                                                                                                                                                                                                                            CAAGAACCAGTTCTCCCTGAAGCTGAGGTCTTGTGAGCCGCCGCAGACACGGCTGTGTTTA 298
                                                                                                                        CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTA---ACTGGTGGAC 117
                                                                                                                                         62 CCTGTCCCTCACCTGCACTGTCTCGGTGGCTCCATCAGCAGTAGTTACTACTGGGG 121
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                                                                              GGTCCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGACCTTCGGAGAGC
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                                                                                                                                                                                                                                              1 GGTCCTGTCCCAGCTGCAGCTGCAGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGAC
                                  Gaps
                                .9
 DB 6; Length 362;
Query Match 62.6%; Score 235.2; DB 6; Length Best Local Similarity 89.1%; Pred. No. 2.6e-55; Matches 278; Conservative 0; Mismatches 28; Indels
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ADE28490 standard; cDNA; 364 ADE28490; RESULT 9
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ID ADE28490
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AC ADE2
XX
DT 29-U
DE Human
XX
Immunit immuni

29-JAN-2004 (first entry)

367

250 234

Human anti-CD40 antibody 23-28-1H-D16E mutant VL heavy chain cDNA.

anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-Hy; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; light chain; ss; gene; mutant; 23-28-1H-D16E.

AAQ33035 standard; cDNA; 366

RESULT 10

GICTCCICA 363

355

(revised)
(first entry)

25-MAR-2003 06-MAY-1993

AAQ33035;

AAQ33035 ID AAQ3 XX AC AAQ3 XX DT 25-M

Homo

WO2003040170-A2

15-MAY-2003

08-NOV-2002; 2002WO-US036107.

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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibocterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder combined immunodeficiancy conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody mutant variable region heavy chain cDNA of the invention.
                                                                                                                                                                                     New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 364 BP; 74 A; 108 C; 108 G; 74 T; 0 U; 0 Other;
                                                                                                   Feng X;
                                                                                                     Jia X,
                                                                                                                                                                                                                                                                           Claim 24; SEQ ID NO 97; 177pp; English.
                                                                                                     Corvalan J,
             09-NOV-2001; 2001US-0348980P
                                            (PFIZ ) PFIZER PROD INC (ABGE-) ABGENIX INC.
                                                                                                   Gladue RP,
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A human MAb specifically binding to a surface antigen of cancer cell membrane comprises variable regions of the heavy and light chains having the amino acid sequences of AAR10145-46 respectively, encoded by DNA sequences AAQ33035-36 respectively. (Updated on 25-MAR-2003 to correct PN i, hybridoma; PCR; variable region; constant region; chain; ss. Human monoclonal antibody specific for a cancer cell membrane surface antigen - prepd. from a hybridoma obtd. by cell fusion between human lymphocytes derived from cancer patients and mouse myeloma cells. Sequence 366 BP; 76 A; 105 C; 111 G; 74 T; 0 U; 0 Other; ĸ Ito N, Nagaike MAb 1-3-1 variable region of heavy chain. Claim 17; Page 31 + 18; 37pp; English **,**-Hirakawa 91JP-00158859. 91JP-00158860. 91JP-00158861. (MITU) MITSUBISHI KASEI CORP 92EP-00110841 Tagawa T, antibody; 1, light ch WPI; 1993-001328/01. P-PSDB; AAR30145. heavy chain; 28-JUN-1991; Hosokawa S, 26-JUN-1992; 28-JUN-1991; 30-DEC-1992 EP520499-A1 Monoclonal Synthetic 128 11 61 DD. ઠે

71 ACCTGCGCTGTCTGGTGGCTCTGTCAGCAGTAGTA---ACTGGTGGACCTGGATCCGC 127 CAGCCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACC 187 177 AACTACAACCCGTCCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAG TACTACAACCCGTCCACAAGAGTCGAGTCACCATATCCGTAGACCACGAGAACCAG 237 TICTCCCTGAACCTGAACTCTGTGACCGCCGCGCACACGCCCGTGTATTACTGTGCCAGA 307 TTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGCGAGG 297 GATTGGGCCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACC 367 357 70 09 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGGAAGCCTTCGGAGACCCTGTCCTTC CAGCTGCAGCTGCAGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC CAGCCCCCAGGGAAGGGCTGGAGTGGATTGGGAGTATTTTATA---GTGGGAGCACC Gaps 9 Query Match 62.4%; Score 234.6; DB 2; Length 366; Best Local Similarity 81.0%; Pred. No. 3.9e-55; Matches 299; Conservative 0; Mismatches 64; Indels 6 Grerectes 366 GTCTCCTCA 376 121 188 178 248 238 308 298 368 358 숨 참 음 ठे ద ò 셤 g Ş ò

BP AAZ49608/c ID AAZ49608 standard; DNA; 351

AAZ49608;

(first entry) 07-APR-2000

DNA-1 related to human antibody clone NHS76

treatment; Human antibody clone NHS76; cytostatic; malignant tumour; human histone H1; antibody; intracellular antigen; diagnosis; tumour; cervical; ovarian; prostate; lung; liver; pancreatic;

stomach; ds.

Homo sapiens

WO200001822-A1.

13-JAN-2000.

99WO-GB002123. 02-JUL-1999;

(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

98GB-00014383.

02-JUL-1998;

Jackson H; Holtet TL, Williams AJ, Tempest PR,

WPI; 2000-137204/12.

New specific binding members capable of binding an intracellular antigen, useful in the treatment and diagnosis of tumors.

Disclosure, Page 64; 70pp; English

The present DNA sequence is related to human antibody clone NHS76. NHS76 is useful for targeting the necrotic centres of malignant tumours by binding to human histone H1 and other intracellular antigens. The specific binding members based on the CDRS (complementarity determining regions) of NHS76 can be used in diagnosis and treatment of tumours like cervical, ovarian, prostate, lung, liver, pancreatic, colon and stomach tumours. Note: There is no relevant information regarding this sequence in the specification

Sequence 351 BP; 75 A; 103 C; 99 G; 74 T; 0 U; 0 Other;

Query Match

ä 292 70 CAGGIGCAGCIGCAGGAGTCCGGCCCAGGACTGAAGCCTTCGGAGACCCTGCCTC CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTTCGGAGACCCTGTCCCTC 15; 62.3%; Score 234.4; DB 3; Length 351; llarity 82.0%; Pred. No. 4.4e-55; Conservative 0; Mismatches 51; Indels 15; Similarity Mar. Local St. 300; 351 11 Best Loca Matches 셤

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115 174 TACAACCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTC TACAACCOGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 191

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311 TGGGCCCAAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 370 7 -----rggrcgaagtttgactattggggccaaggcacccrggrcaccgrc A G 54

> 7 RESULT

Mon Jun 21 11:45:41 2004

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us-09-019-441a-3

CCCCCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAAC

RESULT 13 දු දු ሪ 2 2 B 8 8 8 & The present sequence encodes human antibody clone NHS76 heavy chain variable region. This is useful for targeting the necrotic centres of malignant tumours by binding to human histone Hi and other intracellular antigens. The NHS76 VH gene can be used in the construction of expression vectors. The specific binding members based on the CDRs (Complementarity determining regions) of NHS76 can be used in diagnosis and treatment of tumours like cervical, ovarian, prostate, lung, liver, pancreatic, colon and scommach tumours. The antibody is labelled with functional labels such active drugs at the site of a tumour New specific binding members capable of binding an intracellular antigen, useful in the treatment and diagnosis of tumors. Human antibody clone NHS76 VH, VH, heavy chain variable region, cytostatic, malignant tumour; buman histone Hl, antibody, intracellular antigen; diagnosis; treatment; tumour; cervical; ovarian; prostate; lung; liver; pancreatic; colon; stomach; prodrug; ds. Query Match 62.3%; Score 234.4; DB 3; Length 351; Best Local Similarity 82.0%; Pred. No. 4.4e-55; Matches 300; Conservative 0; Mismatches 51; Indels 15; Sequence 351 BP; 74 A; 99 C; 103 G; 75 T; 0 U; 0 Other; Jackson H; Holtet TL, (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY. Human antibody clone NHS76 VH gene AAZ49590 standard; DNA; 351 BP Claim 15; Fig 1; 70pp; English. 99WO-GB002123 07-APR-2000 (first entry) Tempest PR, WPI; 2000-137204/12. P-PSDB; AAY44615. TCCTCA 376 TCTTCA 1 WO200001822-A1 Williams AJ, Homo sapiens 02-JUL-1999; 02-JUL-1998; 13-JAN-2000 9 AAZ49590; 371 જે G

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121 CCCCCAGGGAAGGGCTGGAGTGGATTTGTTCATA---GTGGGAGCACCTAC 177
                                                                                                                                                    311 TGGGCCCAAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 370
298 AAG------TGGTCGAAGTTTGACTATTGGGGCCAAGGCACCCTGGTCACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                              Human, brain expressed exon, gene expression analysis; probe, microarray, Alzheimer's disease, multiple sclerosis; schizophrenia, epilepsy, cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                    Example 4; SEQ ID NO 20398; 650pp + Sequence Listing; English.
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26-MX-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00603408
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00024263.
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Sequence 319 BP; 69 A; 90 C; 96 G; 64 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of invention demonstrates cycostatic, virucide, antibacterial, immunostimulant and anti-HIV
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  Length 319;
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                                           27; Indels
  DB 4;
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Score 233.8; DB 4
Pred. No. 6.2e-55;
0; Mismatches 27
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62.2%;
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                   Best Local Similarity
Matches 276; Conserv
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activities and may be useful for treating a hyperproliferative disorder such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody full length heavy chain cDNA of the invention.
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                                                                                                                                                                                Length 364;
                                                                                                                                                                                                                     55; Indels
                                                                                                                                             Sequence 364 BP; 74 A; 109 C; 107 G; 74 T; 0 U; 0 Other;
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Best Local Similarity 82.7%; Pred. No. 1.1e-54;
Matches 305; Conservative 0; Mismatches 55
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The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV such as cancer, virucide, antibacterial, immunostimulant and anti-HIV such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody full length heavy chain cDNA of the invention.
                                                                           New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.
                                                                                                                                                                                                     Claim 24; SEQ ID NO 61; 177pp; English
WPI; 2003-441521/41.
P-PSDB; ADE28455.
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Sequence 364 BP; 73 A; 108 C; 110 G; 73 T; 0 U; 0 Other;

Ð, 9; Gaps 62.0%; Score 233; DB 9; Length 364; 82.7%; Pred. No. 1.1e-54; Live 0; Mismatches 55; Indels Best Local Similarity 82.73 Matches 305; Conservative Query Match õ

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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHRAACTERITSICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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17, Appl
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101, App
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117, Appl
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119, Appl
121, Appl
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Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Voko HIRAKAWA
APPLICANT: No. 5767246thiko ITO
APPLICANT: SEQUENTION: Gell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth Lind & Ponack
                                                                               Sequence
Seq
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Sequence 3
Sequence 2
Sequence 2
US-08-851-362D-3

US-08-851-362D-11

US-08-851-362D-7

US-08-851-362D-7

US-08-851-362D-7

US-08-851-362D-7

US-08-851-362D-9

US-08-851-362D-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IRM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERIEGE 5.1
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/360,125
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
PILING DATE: June 29, 1992
APPLICATION NUMBER:
PILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
NAME: WALTEN M. CHEEK
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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US-08-450-578-9

Sequence 9, Application US/08450578

PERTENT NO. 883745

APPLICANT: Salks HOSOKAMA
APPLICANT: Tothiak! Trochan
APPLICANT: Tothiak! Trochan
APPLICANT: Tothiak! Trochan
APPLICANT: Worklak! Trochan
APPLICANT: Worklak! Trochan
APPLICANT: Worklak! Trochan
APPLICANT: MACHINE
TILLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TILLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TILLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
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TILLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TILLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
STREET: 800 Fifteenth Street, N.W., #700
CUNTRY: Washington
STREET: 800 Fifteenth Street, N.W., #700
CONFUTER READALE FORM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRET REPLICATION NUMBER: 00/905,534
FILLE DATE: WATCH NUMBER: 00/905,534
FILLE DATE: WATCH NUMBER: 00/905,534
FILLE DATE: WATCH NUMBER:
TELECOMMUNICATION NUMBER:
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SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: LIDEAT
HYPOTHETICAL:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORGANISM:
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FEATURE:
NAME/KEY:
LOCATION:
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                                                      Query Match 63.2%; Score 237.8; DB 1; Length 3 Best Local Similarity 81.6%; Pred. No. 1.6e-65; Matches 301; Conservative 0; Mismatches 62; Indels
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FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-9
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                                            HYPOTHETICAL:
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US-09-014-880-9
Sequence 9, Application US/09014880
Fatent No. 5990277
FENERAL INFORMATION:
TITLE OF INVENTION: HUMAN MONOCICONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF ESCUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoch, Lind & Ponack, L.L.P.
STATE: D.C.
CONTEX: US.A.
CONTEX: US.A.
STATE: D.C.
CONTEX: US.A.
CONTEX: LEM COMpatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: LEM COMpatible
OFFRATION SYSTEM: W8-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: Danuary 28, 1998
CLASSIFICATION MUMBER: 08/450,578
FILING DATE: Danuary 28, 1995
FILING DATE: Danuary 28, 1994
FILING DATE: Danuary 28, 1995
FILING DATE: Danuary 28, 1995
FILING DATE: Danuary 28, 1994
FILING DATE: Danuary 28, 1995
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                                                                                                                          Length 366;
   ; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1 US-09-017-628-9
                                                                                                                  Query Match 63.2%; Score 237.8; DB 2; Length Best Local Similarity 81.6%; Pred. No. 1.6e-65; Matches 301; Conservative 0; Mismatches 62; Indels
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Pred. No. 1.6e-65;
0; Mismatches 62; Indels 6
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US-09-017-628-9

Sequence 9, Application US/09017628

Patent No. 5990287

GENERAL INFORMATION:

APPLICANT: HOSCAMA, Saiko

APPLICANT: HARAKAMA, Saiko

APPLICANT: HARAKAMA, Voko

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPERITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPERITLE OF INVENTION: SURREACE ANTIGEN OF CANCER CELL:

TITLE OF INVENTION: SURREACE ANTIGEN OF CANCER CELL:

CURRENT APPLICATION NUMBER: US/09/017,628

CURRENT APPLICATION NUMBER: US/09/017,628

CURRENT FILING DATE: 1994-12-20

MUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

LENGTH: 366

TYPE: DNA

ORGANISM: UNKNOWN

FEATURE:
IDENTIFICATION METHOD:

OTHER INFORMATION:
FUBLICATION INFORMATION:
TITLE:
JOURNAL:
JUING DATE:
JOURNAL:
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JUI
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Best Local Similarity 81.6%;
Matches 301; Conservative (
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDFETCH 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: MAY 25, 1995
CLASSIFFCATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION NUMBER: 09/965,534
FILING DATE: December 20, 1994
PRIOR APPLICATION NUMBER: 07/965,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WARTER M. Check, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
REJEPHONE: 202-371-8850
TELEFPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INPORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
FOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANELLE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
CHOMOSOME/SECHENT:
MAP POSITION:
UNITS:
FRATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION:
OTHER INFORMATION:
PUBLICATION INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-450-363-9
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US-08-450-363-9
I US-08-450-363-9
I Sequence 9, Application US/08450363
I Sequence 9, Application US/08450363
I Patent No. 6436434
I GENERAL INFORMATION:
I APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 64364341hiko ITO
APPLICANT: No. Epecifically Binding to Surface Antigen of Cancer
ITILE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
ITILE OF INVENTION: Lind & Ponack
ADDRESSER: Wenderoth, Lind & Ponack
ITY: Wenderoth, Lind & Ponack
STREET: BOS Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, S.25 inch, 500 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 GATTGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC 367
298 GGGAGCTACGGGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 AACTACAACCCGTCCTCAAGAGTCGAGTCATTTTCACAAGACAGGTCCAAGAACAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 TACTACAACCGTCCTCAAGAGTCGAGTCACCATATCCGTAGAACTCAAGAACCAG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 CAGCTGCAGCAGCAGCACCCCAGGAGTGCTGAAGCCTTCGGAGACCTTGTCCCTC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGCTGCAGCTGCAGGAGTCGGGGCCCAGGAGCTGGGAGAGCCTTCGGAGACCCTGTC 60
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.2%; Score 237.8; DB 2; Length 366; Best Local Similarity 81.6%; Pred. No. 1.6e-65; Matches 301; Conservative 0; Mismatches 62; Indels 6
                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: cDNA
) ONICHIAL SOURCE:
) CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-9
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8250
TELEFAX: 202-721-8250
                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 GICTCCICA 376
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STRAIN:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
63.2%; Score 237.8; DB 4;
Best Local Similarity 81.6%; Pred. No. 1.6e-65;
Matches 301; Conservative 0; Mismatches 62;
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ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTA---ACTGGTGGACCTGGATCCGC 127
                                    61 ACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTAGTAGTAGTACTACGGGGCTGGATCCGC 120
                                                                                                                            CAGCCCCCAAGGGAAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACC 187
                                                                                                                                                          121 CAGCCCCAGGGAAGGGCTGGAGTTGGAAGTATCTATTATA---GTGGGAGGACC 177
                                                                                                                                                                                                                                              188 AACTACAACCCGTCCCTCAAGAGTCGAGTCATTTTCACAAGACACGTCCAAGAACCAG 247
                                                                                                                                                                                                                                                                                      178 TACTACAACCGTCCCTCAAGAGTCGAGCACCATATCCGTAGACAGGTCCAAGAACCAG 237
                                                                                                                                                                                                                                                                                                                                                                              TICTCCCTGAACCTGAACTCTGTGACCGCGGGGACACGGGCCGTGTATTACTGTGCCAGA 307
                                                                                                                                                                                                                                                                                                                                                                                                                      238 TICTCCCCTGAAGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGCGAGG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATTGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGGCCAGGGAAGTCCTGGTCACC 367
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US-08-477-553A-46
US-08-477-553A-46
Sequence 46, Application US/08477553A
Sequence 46, Application US/08477553A
Settle No. 59193D.
Settle SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
STATE: 22313-1404
STATE: P.O. Box 1404
STATE: P
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US-08-477-553A-46
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCTCCTCA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 GICTCCTCA 376
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STRANDEDNESS:
TOPOLOGY: line
71
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Query Match 57.9%; Score 217.6; DB 2; Length 372; Best Local Similarity 86.8%; Pred. No. 3.8e-59; Matches 264; Conservative 0; Mismatches 34; Indels 6;

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ACCTGCGCTGTCTATGGTGGGTC---CTTCAGTGGTTACTGGAGCTGGAGCTGCAGTTCGCCAG 117 71 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 130 CCCCCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 190 TACAACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTC 250 234 TCCCTGAACCTGAACTCTGTGACCGCGGGGGGGGGGGGTGTATTACTGTGCCAGAGAT 310 TGGCCCCAAATAGC --- TGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC 367 TIGGACTACATCTCCTTGGATTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC recercaaggregaegrereacegecegeacacegecrererarracrereagagee 294 11 CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 70 1 CAGGTGCAACAACAAGAGGGGGGGGAACAGTTGAAGCCTTGGAAACCCTGTCGG 60 Gaps Sequence 20, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
APPLICANT: OSDOURD:
APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
APPLICANT: MCCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE 53
CORRESPONDENCE 53
CORRESPONDENCE 53
ADDRESSEE: Marshall, O'Toole, Gerstein, Muxray & Borun
STREET: 6300 Sears Tower, 233 South Macker Drive Length 363; STAKET: 6300 Sears Tower, 233 South Wacker DIIVE CITY: Chicage CITY: Chicage CONTRY: Chicage STATE: Illinois COUNTRY: United States of America CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM FC COMPATIBLE OF 57.7%; Score 217; DB 2; Length 36 79.9%; Pred. No. 5.8e-59; ive 0; Mismatches 65; Indels DNA (genomic) Query Match
Best Local Similarity 79.9
Matches 295; Conservative GECTOCTOR 376 Grenderch 363) MOLECULE TYPE: US-08-477-553A-50 US-08-652-816A-20 61 131 191 235 311 251 295 368 Q D δ 셤 ठे 원 g g ð ò ठे ઠે

APPLICATION NUMBER: GB 9525004.9
FILING DATE: O'D-DEC-1995
PRIOR APPLICATION DATE:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 0'J-UN-1994
ATTORNEY/AGENT INTORMATION:
NAME: DATE O'J-UN-1994
REDISTRATION NUMBER: 28.107
REPERENCE/DOCKET NUMBER: 28.111/33308
TELECOMMUNICATION INFORMATION:

LENGTH: 357 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear

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61 ACCTGCACTGTCTCTGGTGACTC---CATCAGTAGTTACTACTGGAGCTGGATCCGGCAA 117
                                                                                                                                                                                                                                                                                                                 71 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 130
                                                                                                                                                                                                                                                                                                                                                                                                                             131 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 TCCAACCCCTCCCTCAAGAGTCGAGTCACATATCAGGAGACACGTCCAAGAAGGGGGTTC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 CCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCCATTACA---GTGGGAGCACCAAC 174
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APPLICANT: Toshiaki TAGAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRARAWA
APPLICANT: Wo. 5767246iniko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                       1 cageracaderecageagreageeeeeagaeregreaageerreggagaeeeere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 TCCCTGAAGCTGAAGCTCTGTGACCGCCGCGGGACACGGCCGTGTATTACTGTGCGGCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 GGTGCCTA---CGATAATTACGGTATAGACGTCTGGGGCAAAGGCACCCTGGTCACCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 TACAACCCGTCCCTCAAGAGTCGAGTCATTCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 TGGGCCCAAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC
                                                                                                                                                                                                    11 CAGCTGCAGCTGCAGGATCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCTTC
                                                                                                                                          6
                                                                                    Length 357;
                                                                                                                                          Indels
                                                                                 Query Match 56.7%; Score 213.2; DB 2; Best Local Similarity 80.1%; Pred. No. 9.1e-58; Matches 290; Conservative 0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TC 372
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TC 353
, TOPOLOGY:
US-08-652-816A-20
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ADDERSORSE Wanderoth, Lind & Ponack STREIT: 805 #ifteenth Street, N.W., #700 CTTTY: NewInderoth, Lind & Ponack STREIT: 805 #ifteenth Street, N.W., #700 CTTTY: NewInderoth Street, N.W., M.W., M.W.,

Sequence 3, Application US/08450578

Sequence 3, Application US/08450578

Patent No. 5837945

GENERAL INFORMATION:

APPLICANT: Salko HOSOKAWA

APPLICANT: Yobilaki TAGAWA

APPLICANT: Yobilaki TAGAWA

APPLICANT: Yoko HIRAKAWA

APPLICANT: Yoko HIRAKAWA

APPLICANT: Woko HIRAKAWA

APPLICANT: Woko HIRAKAWA

APPLICANT: Woko HIRAKAWA

MUMBER OF ENDURING: Bpecifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Bpecifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Bpecifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Cell Membrane

NUMBER OF ENDURENS: 42

ADDRESSER: Wenderch, Lind & Ponack

STREE: 805 Fitteenth Street, N.W., #700

CITY: Washington

COUNTY: Washington

STREE: D.C.

COUNTY: US.A.

ZIP: 2005

COMPITER READER FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

COMPITER: Branch Momber: US.OS

SOFTWARE: Worderfect S.I.

CURREST APPLICATION DATA:

APPLICATION WHERE: US.OS 4250,578

FILING DATE: Date: 09/360,125

FILING DATE: Date: 29, 1995

PILING DATE: UNPERFORMER: US/905,534

FILING DATE: UNPERFORMER: US/905,534 71 ACCTGCGCTGTCTCTGTGGCTCTGTCAGCA---GTAGTAACTGGTGGACCTGGATCCGC 127 238 TICICCCTGAAGCTGAGCTCTCTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGG 297 128 CAGCCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACC 187 121 cascaccassasasascarasasasasarassarasararatara---sressasasas 177 178 TACTACAACCGTCCCTCAAGAGTCGAGTTACCATATCCCTAGACACGTCTAAGAGCCAG 237 248 TICTCCCTGAACTGTGACCGCCGCGGGCGCGCGGTGTATTACTGTGCCAGA 307 308 GATTGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC 367 298 TCTACCCGACTACGGG-----GGGCTGACTACTGGGGCCAGGGAACAATGGTCACC 348 61 ACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTTGTTGTTTCTACTGGAACTGGATCCGC 189 AACTACAACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAG 11 CAGCTGCAGCAGCAGCAGCCCCAGCAGCAGCGTGAAGCCTTCGGAGACCCTGCCTC Query Match

55.8%; Score 209.8; DB 1; Length 357;

Best Local Similarity 79.1%; Pred. No. 1.1e-56;

Matches 292; Conservative 0; Mismatches 62; Indels 15; Gaps 368 GICICCICA 376 349 Grererren 357 JS-08-450-578-3 ద 8 g ď δ ઇ 쉱 ર્જ 염 ઠે 8

; RELEVANT RESIDUES IN SEQ ID NO: US-08-360-125-3

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                                                                                                                                              367
                                                                                                                                                                                298 TCTACCCGACTACGGG------GGGCTGACTACTGGGGCCAGGAACAATGGTCACC 348
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298 TCTACCCGACTACGGG-----GGGCTGACTACTGGGGCAACCAGGAACAATGGTCACC 348
                                                                          238 TTCTCCCTGAAGCTGAGCTCTCTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CAGCACCCAGGGAAGGCCTGGAGTGGATTGGGTACATCTATTACA---GTGGGAGCACC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
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                                  248 TICICCCTGAACCTGAACTCTGTGACCGCGCGGACACGGCCGTGTATTACTGTGCCAGA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 17/22/2016

SEQUENCE 3, Application US/09017628

PATENT NO. 5990287

GENERAL INFORMATION:

APPLICANT: TAGAWA, Saiko

APPLICANT: TAGAWA, Tochiaki

APPLICANT: TAGAWA, Tochiaki

APPLICANT: HIRAKAWA, Voko

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO

TITLE OF INVENTION: SUREACE ANTIGEN OF CANCER CELL MEMBRANE

TITLE OF INVENTION: SUREACE ANTIGEN OF CANCER CELL MEMBRANE

TITLE OF INVENTION: SUREACE ANTIGEN OF CANCER CELL MEMBRANE

TITLE OF INVENTION: SUREACE ANTIGEN OF CANCER CELL MEMBRANE

TITLE OF INVENTION NUMBER: US/09/017,628

CURRENT APPLICATION NUMBER: US/350,125

EARLIER PILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PALENT NOS: 42

SOFTWARE: PALENT NOS: 2.0

SEQ ID NO 3

LENGTH: 357

LENGTH: 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCA---GTAGTAACTGGTGGACCTGGATCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCTTCACAGACCCTGTCCTC
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                                                                                                                                                 308 GATTGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAAGTCCTGGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-3
                                                                                                                                                                                                                                                                                                      349 GTCTCTTCA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-017-628-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 ACCIGCGCIGICICICGGGGCICTGICAGCA---GIAGIAACTGGIGGACCTGGATCCGC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCCCCCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGCCACC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 AACTACAACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACTACAACCCGTCCCTCAAGAGTCGAGTTACCATATCGCTAGAGACACGTCTAAGAGCCAG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTC 60
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STRAIN:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human:
CELL TYPE: Hybridoma producing human:
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
ILBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGNENT:
MAP POSITION:
UNITS:
CONIC STATURE:
ILCATION:
UNITS:
COTHER INFORMATION:
DENTIFICATION INFORMATION:
COTHER INFORMATION:
DENTIFICATION INFORMATION:
SULICATION:
COTHER INFORMATION:
COLUME:
COCUMENT:
CO
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKST NUMBER:
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELERAK:
TELEK:
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENTH: 357 base pairs
TYPE: mucleic acid
STRANBENESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHERICAL:
ANTER CENTER
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
TEMOTH: 357 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGNETT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
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INDIVIDUAL ISOLATE:
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  Sequence 3, Application US/09014880

Patent No. 5950297

Patent No. 5950297

Patent No. 5950297

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIGEN OF CANCER CELL MEMBRANE

NORRESPONDENCE ADDRESS: 4

CORRESPONDENCE ADDRESS: 4

CORRESPONDENCE ADDRESS: 4

CORPERED WASHINGTON NO. 1. ind & Ponack, L.L.P.

ZITY: Washington Compatible Form:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: READABLE FORM:

MCONFUTER: BEN COMPATA: MS-DOS

SOFTWARE: Wachold SYSTEM: MS-DOS

SOFTWARE: Wachold SYSTEM: WS-DOS

SOFTWARE: WATCHION NORRE: US/09/014,880

FILING DATE: January 28, 1998

FILING DATE: January 28, 1998

FILING DATE: December 20, 1994

PRIOR APPLICATION NUMBER: 08/36,125

FILING DATE: UNFORMATION:

REFERENCE/DATE: Warren N. Check, Jr.

REFERENCE/DATE: Warren N. Check, Jr.

REFERENCE/DATE: WARRE: 33,367

REFERENCE/DATE: UNFORWATION:

TELECOMMUNICATION NUMBER: 33,367

REFERENCE/DATE: UNFORWATION:

TELECOMMUNICATION NUMBER: 33,367

REFERENCE/DATE: WARREN 33,367

TELECOMMUNICATION NUMBER: 33,367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL TYPE: Hybridoma producing human CELL TYPE: antibody GAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPCLOGY: linear
MOLECTLE TYPE: CDNA
ORIGINAL SOURCE:
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US-Geguence 3. Application US/08450363
| Sequence 3. Application US/08450363
| Patent No. 6436444
| GENERAL INFORMATION:
| APPLICANT: Saids HEARAMA |
| APPLICANT: Totakishi TAGAMA |
| APPLICANT: You of 36434414hiso Indone
| TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer INTEL OF INVENTION: Specifically Binding to Surface Antigen of Cancer INTEL OF INVENTION: Specifically Binding to Surface Antigen of Cancer INTEL OF INVENTION: Specifically Binding to Surface Antigen of Cancer INTEL OF INVENTION: Specifically Binding to Surface Antigen of Cancer INTEL OF INVENTION: Specifically Binding to Surface Antigen of Cancer STREE: 805 Fifteenth Street, N.W., #700
| CITY: Washington Signature Street, N.W., #700
| CITY: Washington Street, S. Sinch, Soo kb COMPUTER: Intel Machine Machin
                                                                                                                           238 TTCTCCCTGAAGCTGAGCTCTCTGACTGCCGCGGACACGGCCCGTATTACTGTGCGAGG 297
                                                                                                                                                                                                                                                       308 GATTGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACC 367
                                                                                                                                                                                                                                                                                                           298 TCTACCCGACTACGGG------GGGCTGACTACTGGGGCCAGGGAACAATGGTCACC 348
178 TACTACAACCCGTCCCTCAAGAGTCGAGTTACCATATCGCTAGACACGTCTAAGAGCCAG 237
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us-09-019-441a-3_copy_48_423.rni

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APPLICANY: Mocafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBERS OF SEQUENCES. S.
CORRESPONDER. B. DECENTION: Marker Drive
STREET: G000 Sears Tower, 233 South Wacker Drive
GTTREET: G100 Sears Tower, 234 Mar. 1996
GTTREET: G100 Sears Tower, 234 Mar. 1996
FTLING DATE: G12-Mar. 1996
FTLING DATE: G12-Mar. 1992
FTLING DATE: G12-Mar. 1992
FTLING DATE: G12-Mar. 1992
FTLING DATE: G13-Mar. 1992
FTLING DATE: G13-Mar. 1992
FTLING DATE: G13-Mar. 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGGGGCCACC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 TICTCCCTGAACCTGAACTCTGTGACCGCCGGGGCACACGGCCGTGTATTACTGTGCCAGA 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCTGTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 CAGCIGCAGCIGCAGGAGICGGAGGAGIGGIGAAGCCTTCGGAGACCCTGICCCIC
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DEVELOPMENTAL STAGE:
TAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
FOSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
MAP POSITION:
CHROMOSOME/SEGMENT:
MAP POSITION:
CHROMOSOME/SEGMENT:
MAP FOSITION:
ONITS:
PEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
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PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-563-3
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US-08-652-816A-23
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JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
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                                                                                    11 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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  Length 354;
Query Match 55.6%; Score 209.2; DB 2; Best Local Similarity 77.9%; Pred. No. 1.6e-56; Matches 282; Conservative 0; Mismatches 68;
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Sequence 23, Application US/08652816A Patent No. 587215 GENERAL INFORMATION: APPLICANT: Osbourn, JK APPLICANT: Allen, DJ

us-09-019-441a-3_copy_48_423.rni

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Search completed: June 19, 2004, 07:32:31
Job time : 64 secs
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OTHER INFORMATION: /label= CDR2
FEATURE:
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298 GAG------CCTACCGCCAACTTTGATTCTTGGGGCAGCGCCACGCTCACCGTC 348
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238 TTCCTGAGGCTGACTTCTGTGACGCCGCGGGACACGGCCGTTTATTACTGTGCGAGATCT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITZE.
APPLICANT: MARGARITZE.
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION: SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ALLINGTON
STATE: VA
COUNTRY: USA
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LOCATION: 1..369
LOCATION: | 1..369
LOCATEN INFORMATION: /product= "IMMUNOGLOBIN VARIABLE
OTHER INFORMATION: REGION"
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ZIP: 22202

COMPUTER FADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPA:
COMPUTER: IBM PC COMPA:
COMPARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIPICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN P.
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUTCATION INFORMATION:
TTELECOMMUTCATION 
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NAME/KEY: misc_feature
LOCATION: 91.105
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US-08-793-450-3
Sequence 3, Application US/08793450
; Patent No. 6312690
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61 ACCIGCACTGICTAIGGIGGGTC---CTTCAGIGGTTACTGAAGCTGGAICCGCAG 117
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                                                                                                                                              Length 369;
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NAME/KEY: misc_feature

LCCATION: 292..336

// OTHER INFORMATION: /standard_name= "CDR3"

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US-10-309-762-208
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                                                                                                                                                          June 19, 2004, 07:02:32; Search time 283 Seconds (without alignments) 6086.536 Million cell updates/sec
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376
1 ggrcctgtcccagctgcagc......tcctggtcaccgtctcctca 376
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| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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6 US-10-309-762-118
6 US-10-309-762-118
6 US-10-309-762-206
7 US-10-038-591-33
7 US-10-038-591-37
7 US-10-38-214A-37
7 US-10-38-214A-37
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6 US-10-309-762-183
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7 US-09-864-761-83
6 US-10-309-762-196
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                                                                                                                                                                                                                                                                                                                                                                                                              3017426 seqs, 2290544650 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 376
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Perfect score:
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Sequence 65, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 12, Appl
Sequence 27, Appl
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Sequence 21, Appl
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Publication No. US20040018198A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

APPLICANT: Handa, Masahisa

APPLICANT: Handa, Masahisa

APPLICANT: Handa, Masahisa

APPLICANT: ANYDENIES

TITLE OF INVENTION: ANYIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: ANYIBODIES

FILE REPREBRUCE: ABGENIX: 027A

CURRENT FILING DATE: 2002-12-02

PRIOR FILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 246

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 208

LENGTH: 361

TYPE: DNA
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6 US-10-309-762-203
3 US-10-292-088-65
3 US-10-292-088-65
3 US-10-292-088-81
6 US-10-392-088-81
6 US-10-392-088-81
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9 US-10-392-135
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311 TGGGCCCAAATAGCTGGAACGCTAGGCTTCTGGGGCCAGGGGGTCACCGTC 370
295 GGGCAGTGGCTGGAAGACTACGGTATGGACGTCTGGGCCAAGGGACCACGGTCACGGTC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 TACAACCCGTCCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 250
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9
                                                                              RESULT 3
US-10-309-762-182
US-10-309-762-182

Sequence 182, Application US/10309762

Publication No. US20040018198A1

GENERAL INFORMATION:
APPLICANT: Usuan
APPLICANT: Folts, Jan
APPLICANT: Folts, Jan
APPLICANT: GAIlo, Michael

ITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
ITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

STATUM ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

SOUTHAND ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

NUMBER OF ESCOLO NUMBER: 06/337275

PRIOR APPLICATION NUMBER: 06/337275
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65.4%; Score 246; DB 16; Length 361;
Best Local Similarity 83.3%; Pred. No. 6.6e-67;
Matches 305; Conservative 0; Mismatches 55; Indels
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US-10-309-762-206
Sequence 206, Application US/10309762
Sequence 206, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Ghdas, Usan
APPLICANT: Flanda, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE:
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Homo sapiens
US-10-309-762-182
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                                                                                                                                                                                                                                                                                   311 TGGGCCCAAATAGCTGGAACAACCTACGGCTCTGGGGCCAGGGAGTCCTGGTCACGTC 370
295 CAGGGATTTTTGGAGTGGTACCTCTGGACGTCTGGGGCCAAGGGACCACGGTCACGGTC 354
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65.4%; Score 246; DB 16; Length 361;
Best Local Similarity 83.3%; Pred. No. 6.6e-67;
Matches 305; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 118, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Gudas, Jean
; APPLICANT: Gulas, Jean
; APPLICANT: Gala, Michael
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; TITLE OF INVENTION: UNBER: US/10/309,762
; CURRENT APPLICATION NUMBER: 60/337275
; RECOR APPLICATION NUMBER: 60/337275
; RECOR APPLICATION NUMBER: 2001-12-03
; NUMBER: OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-118
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Sequence 57, Application US/10038591
| Sequence 57, Application US/10038591
| Sequence 57, Application No. US20040086503A1
| GENERAL INFORMATION:
| APPLICAMT: Cohen, Bruce D. | APPLICAMT: Miller, Penelope E. | APPLICAMT: Moyer, James D. | APPLICAMT: Moyer, James D. | APPLICAMT: Gallo, Michael | TITLE OF INFORMATION: ANTIBODIES TO INSULIN-LIKE GROWTH PACTOR I RECEPTOR | TITLE OF INFORMATION NUMBER: US/10/038,591 | TITLE OF INFORMATION NUMBER: US/10/038,591 | CURRENT FILING DATE: 2002-01-04 | PRIOR APPLICATION NUMBER: 60/259,927 | PRIOR PILING DATE: 2001-01-05 | NUMBER: OF SEQ ID NOS: 60 | SOFTWARE: Patentin Ver. 2.1 | SEQ ID NO 57 | LEMCHH: 358 | TURNES DATE AS A DELICAME SECOND NOT SEQ ID NOS: 00 | SOFTWARE: PATENT NOS: 00 | SOFTWARE: PATEN
                                                                                                                                                                                                                  131 CCCCCAGGGAAGGGACTGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAAC 190
                                                                                                                                                                                                                                                                                                                                           121 cccccagggaagggcriggaggggaricgggaahcrara---Grigggaggaccaac 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAAGACCAAGAACCAGTTC 237
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                                                                              1 CAGGIGCAGCIGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTC
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ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Consensus
OTHER INFORMATION: sequence
NAME/KEY: modified_base
LOCATION: (337)
OTHER INFORMATION: 4, c, t, g, other or unknown
US-10-038-591-57
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Publication No. US20040086503A1

GENERAL INFORMATION

APPLICANT: Cohen, Bruce D.

APPLICANT: Beebe, Jean

APPLICANT: Moyer, James D.

APPLICANT: Gallo, Michael

APPLICANT: Gallo, Michael

TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR

TITLE OF INVENTION: ANTIBODIES TO JOSULIN-LIKE GROWTH FACTOR I RECEPTOR

TITLE OF INVENTION: ANTIBODIES TO JOSULIN-LIKE GROWTH FACTOR I RECEPTOR

TITLE OF INVENTION: ANTIBODIES TO JOSULIN-LIKE GROWTH FACTOR I RECEPTOR

FILE REFERENCE: ABX.PP2

CURRENT FILING DATE: 2002-01-04

PRIOR PILING DATE: 2002-01-05

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                         Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                              55; Indels
                                                                                                                                                                                                                                                                                                                                                                            Query Match
65.4%; Score 246; DB 16;
Best Local Similarity 83.3%; Pred. No. 6.6e-67;
Matches 305; Conservative 0; Mismatches 55;
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/33725
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 206
LENGTH: 361
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Best Local Similarity 90.3
Matches 270; Conservative
                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-309-762-206
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ORGANISM: Homo sapiens
US-10-038-591-33
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LENGTH: 296
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APPLICANT: Basi, Guriq
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
TITLE OF INVENTION: ANYLOID PEPTIDE
TITLE OF INVENTION: ANYLOID PEPTIDE
FILE REPERENCE: ELN-004
CURRENT PELING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/363,751
PRIOR RILING DATE: 2002-03-12
NUMBER OS SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH. 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             crereceacaca 356
                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: (1)...(356)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: sig_peptide
; LOCATION: [1]...(57)
US-10-388-214A-37
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                                                             311 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACGTC 370
292 ACGATTTTTGGAGTGGTATTATCTTTGACTACTGGGGGCCAGRGANCCCTGGTCACGTC 351
TCCCTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGCCAGAGAT 310
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                 Gaps
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US-10-388-214A-35

Sequence 35, Application US/10388214A

Sequence 35, Application US/10388214A

Sequence 35, Application US/10388214A

SEMERAL INFORMATION:
GREEAL INFORMATION:
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA

TITLE OF INVENTION: AMTLOID PEPTIDE

TITLE OF INVENTION: AMTLOID PEPTIDE

CURRENT APPLICATION NUMBER: US/10/388,214A

CURRENT APPLICATION NUMBER: US/10/388,214A

CURRENT APPLICATION NUMBER: US/10/388,214A

PRIOR FILING DATE: 2002-03-02

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 35

LENGTH: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 235.2; DB 17; Length
Pred. No. 1.6e-63;
0; Mismatches 28; Indels
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Best Local Similarity 89.1%;
Matches 278; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
US-10-388-214A-35
                                                                                                                               TCCTCA 376
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Pank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL, FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERBYCE: Aeomica -K-1
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
                                                                                                                                                                                                        107
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                                                                                                                                                                                                                                                                    61 CCTGTCCCTCACCTGCGCTGTCTCTGTGGCTCTGTCAGCAGTAGTA---ACTGGTGGAC 117
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                                                                                                                                                                            GETCCTGTCCCAGCTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 TGGGGCCACCAACTACAACCGGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTC
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       DB 17; Length 356;
                                                                      Indels
Score 235.2; DB 17;
Pred. No. 1.6e-63;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32297, Application US/09864761
Patent No. US20020048763A1
   Query Match
Best Local Similarity 89.1%;
Matches 278; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGTGCCAGAGA 309
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RESULT 8 US-10-388-214A-37 ; Sequence 37, Application US/10388214A

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DB 16; Length 367;
                          RESULT 10

US-10-309-762-183

Sequence 183, Application US/10309762

Publication No. US20040018198A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

APPLICANT: Foltz, Ian

APPLICANT: Handa, Masahisa

APPLICANT: Handa, Masahisa

APPLICANT: Gallo, Michael

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

FILE REFRENCES: ABGENIX: 0.27

CURRENT APPLICATION NUMBER: US/10/309,762

PRIOR PLLICATION NUMBER: 06/337275

PRIOR PLLICATION NUMBER: 60/337275

PRIOR PLLICATION NUMBER: 60/337275

PRIOR PLICATION NUMBER: 60/337275

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 183

LENGTH: 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.4%; Score 234.8; DB 16; Length Best Local Similarity 82.8%; Pred. No. 2.1e-63; Matches 308; Conservative 0; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
GRGANISM: Homo sapiens
US-10-309-762-183
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US-10-309-762-196
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122 CTGGATCCGCCAGCAGGGAAGGGCTGGAGTGGATCTATATA---G 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGAACCAGTTCTCCCTGAACCTGAACTCTGTGACCGCGGGACACGGCCGTGTATTA 297
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AB019439.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.43
OTHER INFORMATION: SWISSPROT HIT: P06331, EVALUE 1.00e-28
OTHER INFORMATION: EST HUMAN HIT: AW408410.1, EVALUE 0.00e+00
US-09-864-761-32297
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PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PAPLICATION NUMBER: PCT/US01/00666
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 32297
LENGTH: 362
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131 CCCCCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGGGGCCACCAAC 190
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                                                                                             9
                                                                              1 CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTC
                                                                                                                                                                                                                                                                         118 CCCCCAGGGAAGGGACTGGATTGGGTATATCTATTACA---GTGGGAGCACCACCAAC
                                                                                                                                                                                                                                                                                                                                             TACAACCCGTCCCTCAAGAGTCGAGTCATCATTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 GGGTACGATATTTGACTGGTTATGACTACTTTGACTACTGGGGGCCAGGGAACCCTGGTC
                                                 11 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
  Gaps
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 196, Application US/10309762
Fublication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gadas, Jean
APPLICANT: Galo, Michael
APPLICANT: Handa, Michael
APPLICANT: Gallo, Michael
APPLICANT: Gallo, Michael
APPLICANT: ABGENIX.027A
FILE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT FILING DAIR: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
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                                                                                                                                                                                                                                                                                                                                                                                                                       131 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGTGGGCCACCAAC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                              251 TCCCTGAACCTGAACTCTGTGACCGCGCGCGCCGCCGTGTATTACTGTGCCAGAGAT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 TGGGCCCAAAT----AGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTC 364
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                                                                                                                                                                                                                                                                                                1 CAGGIGCAGCIGCAGGAGICGGGCCCAGGACIGGAGGCCTICGGAGACCCTGICCCTC 60
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                                                                                                                                                                              Query Match 62.4%; Score 234.8; DB 16; Length Best Local Similarity 82.8%; Pred, No. 2.1e-63; Matches 308; Conservative 0; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.4%; Score 234.6; DB 13; Length 82.9%; Pred. No. 2.46-63; ive 0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQUENCE 108 APPLICATION US/10292088
PUDJICATION NO. US20030211100A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: GLADUE, RONALD P.
APPLICANT: JAA, XIAO-HI
APPLICANT: JAA, XIAO-HI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: 60/348,980
CURRENT PILING DATE: 2003-03-14
FRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 97
LENGTH: 34
TYPE: DNA
ORGANISM: Homo sapiens
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 196
LENGTH: 367
TYPE: DMA
ORGANISM: Homo sapiens
US-10-309-762-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 82.9°
Matches 306; Conservative
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US-10-292-088-97
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US-10-292-088-97
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71 ACCTGGGCTGTCTCTGGCTCTCTCAGCAGTAGTAACTGGACCTGGATCCGCCAG 130
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                                                                                                                                                                                              131 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAAC 190
                                                                                                                                                                                                                            118 CCCCCAGGGAAGGAACTGGAGTGGATTGGGTATATTACA---GTGGGAGCACCAAC 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 GGGTACGACTTTTTGACTGGTTATGACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 354
                                          1 CAGGIGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCTTGTTCTCTCCTC
                                                                                                                                                                                                                                                                                  JOSTICATION NO. US20040016198A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Godas, Jean
APPLICANT: Godas, Jean
APPLICANT: Handa, Masshisa
APPLICANT: Golas, Jean
APPLICANT: Golas, Jean
APPLICANT: Golas, Jean
APPLICANT: Golas, Jean
APPLICANT: Godas, Jean
APPLICANT: Golas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC AMHYDRASE IX
ITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC AMHYDRASE IX
ITLE OF INVENTION: ANTIBODIES AGAINST APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-03
NUMBER: OF SEC ID NOS: 246
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 181
LENGTH: 367
TYPE: DNA
CNGANISM: Homo sapiens
US-10-309-762-181
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US-10-309-762-181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GATCCGCCAGCCCCCCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGTGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACCAGTTCTCCCTGAACCTGAACTCTGTGACGGCGGGGGGACACGGCCGTGTATTACTG 300
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                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
CTHER INFORMATION: MAP TO AB019438.1
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
CTHER INFORMATION: NT HIT: U03896.1, EVALUE 0.00e+00
CTHER INFORMATION: EST HUMAN HIT: AW402332.1, EVALUE 0.00e+00
CTHER INFORMATION: SWISSPROT HIT: P06331, EVALUE 3.00e-36
US-09-864-761-28401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 116, Application US/10309762
; Publication No. US20040018198A1
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
APPLICANT: Handa, Masahisa
APPLICANT: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
ITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT PILING DATE: 2002-12-02
} RICH PILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FESESEQ for Windows Version 4.0
; SEQ ID NO 116
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION WUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
ENGTH: 319
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US-10-309-762-116
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71 ACCTGCGCTGTCCTCGTCGCTCTCTCTCTCAGAGAGTAGTAACTGGTGGACCTGGATCCGCCAG 130
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                                                                                                                                                                                                            118 CCCCCAGGGAAGGGACTGGACTGGTATATCTATTACA---GTGGGAGCACCAAAC 174
                                                                                          9
                                                                                                                                           131 CCCCCAGGAAGGACTGGAGTTGGACGTATTCTCTGGTAGTGGTGGGCCACCAAC
                                                                            11 CAGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCATCGCAAAGCCTTCGGAGCCCTGTCCCTC
                                                                                                                                                                                                                                                191 TACAACCCGTCCTCAAGAGTCGAGTCATTTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                                              Gaps
                                12;
Query Match
62.0%; Score 233.2; DB 16; Length 367;
Best Local Similarity 82.5%; Pred. No. 6.7e-63;
Matches 307; Conservative 0; Mismatches 53; Indels 12;
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Gaps

Query Match
62.0%; Score 233.2; DB 16; Length 367;
Best Local Similarity 82.5%; Pred. No. 6.7e-63;
Matches 307; Conservative 0; Mismatches 53; Indels 12;

; TYPE: DNA ; ORGANISM: Homo sapiens US-10-309-762-116

Search completed: June 19, 2004, 08:16:39 Job time: 285 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

June 19, 2004, 06:19:02; Search time 1733 Seconds (without alignments) 6479.042 Million cell updates/sec Run on:

US-09-019-441A-3_COPY_48_423 376

1 ggtoctgtoccagotgcago.....toctggtcacogtotcctca 376 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

27513289 seqs, 14931090276 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 376

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

EST:*

1: em_estba:;

2: em_esthum:;

4: em_estion:;

4: em_estion:;

5: em_estov:;

6: em_estov:;

7: em_estion:;

7: em_estion:;

8: gb_esti:;

9: gb_esti:;

9: gb_esti:;

1: gb_esti:;

1: gs_em_estion:;

1: em_gss_fun:;

2: em_gss_fun:;

2: em_gss_fun:;

3: gss_fun:;

4: em_gss_fun:;

5: em_gss_fun:;

6: em_

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		AW403845 UI-HP-BK0	AW405472 UI-HF-BL0	AW404242 UI-HF-BL0	AW402748 UI-HF-BK0
	ΩI	******	AW403845	AW405472	AW404242	AW402748
	œ,	3	10	10	10	10
	Query Match Length DB	1 1 1 1	374	319	369	370
ф	Query Match i	1 1 1 1	60.7	59.7	58.2	57.9
	Score		228.4	224.6	218.8	217.8
	Result No.	111111	H	7	m	4

AW401544 UI-HF-BKO AW401636 UI-HF-BKO AW403420 UI-HF-BKO AW40389 UI-HF-BKO BM820975 K-BST0089 AW732986 bb18e10.Y BI225611 602948938 AW503256 UI-HF-BNO	140 CM1-CN 336 EST208 336 EST208 330 CM0-HT 180 BP4324 319 UI-HF- 155 MR1-ET- 157 MR1-ET- 181 CM4-HT	7860 ILS-ENOO 1875 K-EST013 2075 KO-CNOO 9898 MR1-ET01 1855 K-EST013 34470 PM4-UT01 1844 PM4-UT01 185 EST69374 538 UI-HF-EK 1812 PM3-CT05 1812 PM3-CT05 1812 PM3-CT05 1813 MR4-SNOO 1814 MR4-SNOO 1814 MR4-SNOO 1814 MR4-SNOO 1814 MR4-SNOO 1814 MR4-SNOO 1815 EST56382 1894 MYE4006 I 1855 EST26382 1894 MYE4006 I 18585 EST26382 1894 MYE4006 I 18585 EST26382 1894 MYE4006 I	59893 MR1-ETO 03007 UI-HF-E 99993 MR3-HNO
10 AW40 10 AW40 10 AW40 12 BW40 12 BW78 10 AW750	0 4 0 0 7 0 0 0 0 0	10 BF84 10 AW86 11 BF88 11 BF88 12 BF88 14 CD56 12 BF70 12 BF70 14 CD56 10 AW86 10 AW86 11 AW8	10 BF869 10 AW403 12 BG999
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55 21 6 216. 7 215. 8 212. 9 208. 1 207.	22 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		3 161 5 161

ALIGNMENTS

	AW403845 374 bp mRNA linear BST 16-FEB-2000	UI-HF-BK0-abl-h-02-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone	IMAGE:3056859 5', mRNA sequence.	AW403845	AW403845.1 GI:6922998	EST.	Homo sapiens (human)	Homo sapiens	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Buthería; Primates; Catarrhini; Hominidae; Homo.	(bases 1 to 374)	NIH-MGC http://mgc.nci.nih.gov/.	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)	Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov	Eco RI site shown at the beginning of the sequence.	issue Procurement: Louis M. Staudt, M.D., Ph.D.	cDNA Library Preparation: M.B. Soares Lab	cDNA Library Arrayed by: M.B. Soares Lab	DNA Sequencing by: M.B. Soares Lab	Cone distribution: MGC clone distribution information can be	found through the I.M.A.G.E. Consortium/Linn at:	www-bio.llnl.gov/bbrp/image/image.html	sed primer: Mis Forward.
RESULT 1 AW403845		DEFINITION U		ACCESSION A	VERSION	KEYWORDS E	SOURCE	ORGANISM	4	2.	REFERENCE 1	AUTHORS	TITLE	JOURNAL C	COMMENT	щ	щ						44	,3 C	/1

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PEATURES
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                                 /organism="Homo sapiens"
/mol_type="mkNA"
/db_xref="t_axon:9606"
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/clone="IMAGE:3056859"
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/coll type="mylim MGC 36"
/note="vector: pry13-pac; Site_1: NotI; Site 2: Bco RI;
/constructed from size fractionated cytoplasmic mRNA
/constructed from size fractionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW405472 319 bp mRNA linear EST 16-FEB-2000 UI-HF-BL0-adh-d-02-0-UI.rl NIH MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGGCCACCAACTACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACAGGTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGGAACACCTACTATAACCCGTCCCTCAAGAGTCAAGTCACCATATCCGTAGACACGTC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGTCCCTCACCTGCGCTGTCTCTGTCACCACTAGTA---ACTGGTGGAC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGATCCGCCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases I to 319)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGTCCTGTCCCAGCTGCAGCTGCAGGAGTCGGCCCAGGAGTGGTGAAGCCTTCGGAGAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 GGTCCTGTCCCAGCTGCAGCTGCAGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGAC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Sco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                           6; Gaps
                                                                                                                                                                                                                                                                                                                                                     Length 374;
                                                                                                                                                                                                                                                                                                                                                   60.7%; Score 228.4; DB 10; Length 86.8%; Pred. No. 6.1e-49; ive 0; Mismatches 36; Indels
Location/Qualifiers
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Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

B. (Dases 1 to 369)

NH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Eco R site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: W.B. Soares Lab

DNA Sequencing by: W.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 bp mRNA linear EST 16-FEB-2000
UI-HF-BLO-abq-f-09-0-UI.rl NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3057545 5', mRNA sequence.
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(1.5-2.Shb) Directionally cloned Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Location/Qualifiers

Seq primer: M13 Forward

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UI-HF-BKO-abf-d-09-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3055937 5', mKNA sequence.
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NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Realth, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.

Email: cgapbe-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab
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found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward.
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/cell_line="MGGS"
/lab_Engler="BH10B (LTI)"
/lab_Engler="BH10B (LTI)"
/clone_lib="NHH MGC 37"
/note="Vector: PT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(1.5-2:5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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UI-HF-EKO-aak-d-08-0-UI.ri NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3054014 5', mRNA sequence.
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Bukaryote, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 370)
1 (bases 1 to 470)
1 Nath-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Enail: cgapbs-r@mail.nih.gov
Eco Ri site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arxayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
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Pred. No. 1.9e-46;
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              www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
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58.2%; Score 218.8; I
Best Local Similarity 84.9%; Pred. No. 1.9e-
Matches 270; Conservative 0; Mismatches
                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="INAGE:3057545"
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| organism="McMon sapiens" |
| wol_type="mRNR" |
| clone="TMAGE:3055937" |
| tissue_type="germinal center B cells" |
| cell_line="MGC85" |
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UI-HF-BKO-aae-d-03-0-UI.rl NIH_MGC_36 Homo sapiens CDNA clone
IMAGE:3053596 5', mRNA sequence.
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11. HarMGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/lmage.html
Seq primer: M13 Forward.
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Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
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83.1%; Pred. No. 5.7e-46;
iive 0; Mismatches 51;
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AW401636
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/db_xref="taxon:9606"
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UI-HF-BKO-abe-g-03-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3056068 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 363)
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        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Porward.
Location/Qualifiers
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                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
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57.7%; Score 216.8; DB 10; Length

Best Local Similarity 86.0%; Pred. No. 6.3e-46;

Matches 265; Conservative 0; Mismatches 37; Indels
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FEATURES

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Location/Qualifiers

1. 368
| organism="Homo sapiens" |
| Organism="Homo sapiens" |
| Ab xref="Laxon:9606" |
| Clone="IMAGE:3056679" |
| Clone="IMAGE:3056679" |
| Call type="germinal center B cells" |
| Canstructed from size fractionated cytoplasmic mRNA |
| Constructed from size fractionated cytoplasmic mRNA |
| Catudt, Ph. D. Inbrary preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. |
| Bonaldo, Ph.D. and M. Bento Soares, Ph.D. |
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 358)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at: Seq primer: M13 Forward.
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Unpublished (2002)
Contact: Kim YS
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Kim, Y.S.
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246 TAAGAACCAGTTCTCCCTGAAGCTGAACTCTGTGACTGCCGGGACACGGGCGGTGTATTA 305
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      cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGTCCTGTCCCAGCTGCAGCTCGAGGAGTCGAGGAGTGGTGAAGCCTTCGGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.2%; Score 215.2; DB 10; Length 363; llarity 85.4%; Pred. No. 1.7e-45; Conservative 0; Mismatches 39; Indels 6;
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Homo sapiens
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KEYWORDS
SOURCE
ORGANISM
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REFERENCE AUTHORS TITLE JOURNAL COMMENT

ACCESSION

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Best Loca Matches

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ORIGIN

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dassolute) (Aug. noi.nih.gov/.

1. (Dayblished (1999)

1. (Dayblished (1999)

1. (Contact: Robert Strausberg, Ph.D.

1. (Bmail: Gapbs-r@mail.nih.gov

1. (Saue Procurement: Louis M. Staudt, M.D., Ph.D.

1. (CDNA Library Preparation: Ling Hong/Rubin Laboratory

1. (CDNA Library Preparation: Ling Hong/Rubin Laboratory

1. (CDNA Library Brayed by: The I.M.A.G.E. Consortium (LIANL)

1. (CDNA Library Mashington University Genome Sequencing Center

1. (Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

1. (CONTROLE) (CONTROLE
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                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="Top10p""
/clone lib="S19N665307"
/clone lib="S19N665307"
/clone lib="S19N665307"
/note="Grgan: Stomach; Vector: pCNS; Site l: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 6 ont. The CDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells B. coli Top10F' by electroporation method. The CDNA libraries constructed by this method are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGTCCCTCACCTGCGCTGTGGCTCTGTCAGCAG---TAGTAACTGGTGGAC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGGTCCGCCAGTCCGCCGGGAAGGGACTGGAGGGGATAGGGCGTATCT---ATACCTA 209
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            Korea Research Institute of Bioscience & Biotechnology 52 Ecenn-dong Yuseong-gu, Daejeon 305-333, South Korea 7el: +82-42-860-4470
Fax: +82-42-860-44409
Email: yongsung@mail.kribb.re.kr
Plate: 9 row: C column: 09
High quality sequence stop: 358.
I.o.aston/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length 358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.5%; Score 208.6; DB 1;
llarity 83.9%; Pred. No. 8.7e-44;
Conservative 0; Mismatches 44
                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGTGCTCGAG 340
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/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" Location/Qualifiers

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/dlone=InAdGE:296224*
/tlssue type="Burkitt lymphoma"
/lab_hot=="DH10B (phage-resistant)*
/lone lib="NH1M (phage-resistant)*
/lone lib="NHM MGC 8"
/note="Organ: lymph, Vector: pCTB7; Site 1: XhoI; Site_2:
Eorgi, cDNA made by oligo-dr priming. Directionally
cloned into Eorgi/Xhoi site using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M: Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI225611 365 bp mRNA linear EST 11-JUL-2001 602948938F1 NIH_MGC_B Homo sapiens cDNA clone IMAGE:5093504 5', mRNA sequence.
BI225611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 ---CACCAACTACAACCGTCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 55.4%; Score 208.4; DB 10; Length Best Local Similarity 84.6%; Pred. No. 1e-43; Matches 259; Conservative 0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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AW732986

374 bp mRNA linear EST 21-APR-2000 bb18e10.yl NIH MGC 8 Homo sapiens cDNA clone IMAGE:2963274 5'
similar to gb:M54911_rnal IG HEAVY CHAIN PRECURSOR V-II REGION (HUMAN); mRNA sequence.
AW732986
AW732986.1 GI:7633328

ACCESSION VERSION KEYWORDS

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EST 12-JAN-2001
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                                                                                                                                                                                                                                                                       NIH-WGC http://mgc.nci.nih.gov/.
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1994)
Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: W.B. Soares Lab
DNA Sequencing by: W.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/lange/lange.html
Seq primer: M13 Porward.
                                                                                                                                                                                  Eukaryotzi, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 340)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="lymph"
/cell type="germinal center B cells"
/cell line="MGCB"
/cell line="MGCB"
/lab host="ParloB (LTI)"
/clone lib="NIH MGC 50"
/note="Vector: PT7T3-pac, Site 1: Not1; Site 2: Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 Gercerereceaecrecaacrecaecaeresesececaeseresesecereaaecerresesese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Constructed from size fractionated cytoplasmic mRNA (3.5-4.4kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria of Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCCTGTCCCAGCTGCAGCAGCAGCAGCAGCCCCAGGAGTGGTGAAGCCTTCGGAGAC
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Best Local Similarity 84.1%; Pred. No. 2e-43;
Matches 259; Conservative 0; Mismatches 43; Indels
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
   IMAGE:3078487 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:3078487"
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                                     AW503526
AW503526.1 GI:7140086
                                                                                                                            Homo sapiens (human)
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// Ardf="Laxon:9606"
// Ardf="Laxon:9606"
// Ardf="Laxon:9606"
// Ab host="DH10B (phage-resistant)"
// Ab host="DH10B (phage-resista
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW503526
UI-HP-BN0-aky-b-04-0-UI.rl NIH MGC_50 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genoatics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llni.gov
Plate: LLCM1860 row: k column: 09
High quality sequence stop: 365.
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                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 365)
11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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   BI225611.1 GI:14679055
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0; Conservative
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                                                                                                 Homo sapiens
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and

CM1-CN0061-131200-642-c02 CN0061 Homo sapiens cDNA, mRNA sequence

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LUJU4336 347 bp mRNA linear EST 25-JUN-2003
EST20863 human nasopharynx Homo sapiens CDNA, mRNA sequence.
CD704336
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                  Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. Zeng,Y.-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/tiseue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/nore="ESTS generated from a normal nasopharynx CDNA
library from southern Chinese"
                                                                                                                                                                                                                                                                                                                                                                     Transcriptional Gene Expression Profile of Human Nasopharynx
                                                                                                                                                                                                                                                         Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
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86.6%; Pred. No. 2.9e-43;
iive 0; Mismatches 34; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer Center
Sun Yat-sen University
51 DongFeng Road Bast, Guang21
Tel: 86-1380-9770-73
Fax: 86-20-8775-4506
Email: yzceng@gseums.edu.cn.
Location/Qualifiers
                                                                                                                                                                                                                                 Homo gapiens
Eukaryota, Metazoa, Chordata,
Eukaryota, Butheria, Primates,
1 (bases 1 to 347)
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                                                                                                                                                               CD704336.1 GI:32234966
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                                                                                                                                                                                                           sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
Contact: YiXin Zeng
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Matches 240; Conserv
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Site_2: Smal; A min_library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - ludwig Institute for Cancer Research)
profiles into the puCl 18 vector: Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                Homo sapiens
Bukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Magazi, Cataria; Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagazi, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,
Brunstein, A., de Silva, W. Jr., Reukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., Geoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Sobotgun sequencing of the human transcriptome with ORF expressed
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Fax: +55-11-2707010

Fax: +55-12-2707010

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Fax: +55-12-2707010

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMl&t2=CMl-CN0061-131200-642-c02&t5=2000-12-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 360.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
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                                                BF767440.1 GI:12115340
                                                                                               Homo sapiens (human)
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Gaps ģ Query Match 54.5%; Score 204.8; DB 10; Length 342; Best Local Similarity 83.7%; Pred. No. 8.4e-43; Matches 256; Conservative 0; Mismatches 44; Indels 6;

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301 TGCCAG 306

337 TGCGAG 342

Search completed: June 19, 2004, 07:31:24 Job time : 1737 secs

Won Jun 71 11:45:42 2004

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compuges Ltd.

June 19, 2004, 04:01:44; Search time 1844 Seconds
(without alignments)
7545.073 Million cell updates/sec US-09-019-441A-5_COPY_67_387 321 1 gacatccagatgacccagtc......ggaccaaggtggaaatcaaa 321 2865150 3470272 seqs, 21671516995 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 1: 9b ba: *
2: 9b lng: *
3: 9b lng: *
4: 9b lng: *
5: 9b lng: *
6: 9b lng: *
7: 9b Minimum DB seq length: 0 Maximum DB seq length: 321 GenEmbl:* Title: Perfect score: Sequence: Scoring table: Searched: Database Run on:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	AJ400402 Homo sapi AJ240111 Homo sapi AJ240111 Homo sapi AJ400420 Homo sapi AF005340 Homo sapi AF00535 Homo sapien AF004451 Synthetic AR161045 Sequence AR161046 Sequence AR161046 Sequence AR161046 Sequence AR161048 Sequence AR160378 Sequence AR160378 Sequence AF00318 Homo sapi AF04456 Sequence AF10383 Homo sapi AF10383 Homo sapi AF10383 Homo sapi AF104456 Synthetic AR161048 Sequence AF104456 Synthetic AR161048 Sequence AF164456 Synthetic AR161048 Sequence AF164456 Synthetic AR161048 Sequence AF16538 Homo sapi AF044447 Synthetic AR160978 Sequence AR160978 Sequence AR16097 Sequence AR16097 Sequence AR16097 Squence AR16097 Squence AR16097 Squence AR16097 Squence AR16097 Squence AR16097 Squence AR16097 Squence AR16097 Squence AR16097 Homo sapi AR30388 Homo sapi	DNA linear PRI 01-AUG-2001 immunoglobulin kappa chain in; immunoglobulin light chain; ata; Vertebrata; Buteleostomi; rhini; Hominidae; Homo. Distel,L. and Grawunder, U.
QI	HSA408402 #X240164 #X243111 #Y240164 #Y32408420 #Y062340 #Y062340 #Y062340 #Y062340 #Y062340 #Y064451 #Y044451 #Y040817 #Y044454 #Y160976 #Y160976 #Y160976 #Y160976 #Y160976 #Y160978 #Y160978 #Y160978 #Y160978 #Y160978 #Y044457 #Y062339 #Y315905 #Y3	320 bp 7. gene for 7. in kappa cha in kappa cha mates; Crani mates; Catax
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Direct Submission
Submitted (04-JAN-2001) Harfst B., Immunologie,
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       patients with Nijmegen
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1. .320
/gene="IGKV"
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       cells from
Normal V(D)J recombination in cells Ebreakage syndrome Mol. Immunol. 37 (15), 915-929 (2000) 21179552 11282395
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AY240164 321 bp mRNA linear PRI 09-APR-2003 Homo sapiens clone HA6 anti-HAV capsid immunoglobulin G light chain Ayzable region mENA, partial cds.

ACCESSION

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1. .321
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variable region"
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KVEIK"
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Homo sapiens partial mRNA for immunoglobulin light chain variable
region (a10 gene).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ATCACTIGCAGGCAAGTCAGGACATTAGGTATTAAATTGGTATCAGCAGAAACCA 120
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                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (20-FEB-2003) Antibody Engineering RU, Korea Research
Institute of Bioscience and Biotechnology, Yusung, Daejon 305-333,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
Homo sapiens (human)

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 321)

Kim,S.J., Jang,M.H., Stapleton,J.T., Yoon,S.O., Jeon,E.-S. and Hong,H.J.

Metralizing Human Monoclonal Antibodies to Hepatitis A Virus Recovered by Phage Display

L Unpublished

E 2 (bases 1 to 321)

Kim,S.J., Jang,M.H., Stapleton,J.T., Yoon,S.O., Jeon,E.-S. and Hong,H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AGGITCAGCGGCAGTGGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCT
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AJ243111.1 GI:5102680
a30 gene; immunoglobulin light chain; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.0%; Score 279.4; DB 9; Length llarity 91.9%; Pred. No. 1.5e-78; Conservative 0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGACCAAGGTGGAAATCAAA 321
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Best Local Similarity
Matches 295; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
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VERSION
KEYWORDS
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LOCUS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL REFERENCE AUTHORS	TITLE JOURNAL	FEATURES	CDS		ORIGIN Ouery Ma		δ	qq	ò	qu	ò	дq	δŏ	ПЪ	ζō	qa	ć	අු	
SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,	heria, Primates, Tengner,P., Levi, nd Wahren-Herlenn n variable genes ti -Ro 52-kd in pr		Elagib, K.E. Direct Submissi	AL Submitted Research, NORWAY	FEATURES Location/Qualifiers 1. 311 source 1. 421 /organism="Homo sapiens" /mol_type="mRNA"	/ darmine / germine gene 1311	variable ERSQGIRNU	/product≈"lmmunog⊥obulin lignt chain variable region" ORIGIN	Query Match 85.1%; Score 273.2; DB 9; Length 311; Best Local Similarity 92.6%; Pred. No. 1.5e-76; Matches 287: Conservative 0: Mismatches 23; Indels 0; Gaps 0;	THE STATE OF THE S	Db 1 GACATCCAGATGCAGTCTCCATCCTCCCTGCATCTGTAGAGACAGAGACACCC 60	Oy 61 ATCACTTGCAGGCAAGTCAGGACATTAGGTATTATATAAATTGGGTATCAGCAGAAACCA 120	Db 61 ATCACTGGGGGAAGTCAGGGCATTAGAATGATTAGGCTGGTATCAGCAGAAACCA 120	Qy 121 GGAAAAGCTCCTAAGCTCCTGATCTATGCTTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180	Db 121 GGGAAAGCCCCTAAGCGCCTGATCTATGCTATCCAGTTTGCAAAGTGGGGTCCCATCA 180	Qy 181 AGGTTCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCGCGGCGGCCT 240	Db 181 AGGTTCAGCGGCAGTGGATCAGAATTCACTCTCACAATCAGCAGCCTGCAGCT 240	Qy 241 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 300	Db 241 GAAGATTTTGCAACTTATTACTGTCTACAGCATAATAGTTACCCTCGGAGGTTCGGCCAA 300	Qy 301 GGGACCAAGG 310	Db 301 GGGACCAAGG 310	RESULT 4	AF329459

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Homo sapiens (human)
Homo sapiens (bundan)
Homo sapiens
Homo sapiens
Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Bukaryota, Metazoa, Chordata; Catarrhini; Hominidae, Homo.

II (bases 1 to 321)
Bull,S., Karle,S., Luo,J., Gololobov,G., Nishiyama,Y., Planque,S.,
Burr,G., Thiagarajan,P., Tramontano,A. and Hanson,C.
Characterization of Lupus Antibodies to a Conserved Epitope of HIV
GP120
Chases 1 to 321)
Equil,S., Karle,S., Luo,J., Gololobov,G., Nishiyama,Y., Planque,S.,
Burr,G., Thiagarajan,P., Tramontano,A. and Hanson,C.
Direct Submission
Submitted (18-DEC-2000) Pathology and Laboratory Medicine,
University of Texas-Houston Medical School, 6431 Fannin, Houston,
TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers

1. 321
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[N (6-biotinylhexanediamin-1-yl)carboxymethyl]tropan-3-ol
diester) and gpl20"
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/translation="GIQMTGSPSSLSASV
AF329459 321 bp mRNA linear PRI 19-MAY-2003
Homo sapiens clone SK-18 recombinant antibody light chain VL domain
mRNA, partial cds.
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>cal Similarity 90.3%; Pred. No. 5.7e-76;
s 290; Conservative 0; Mismatches 31; Indels 0;
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243 AGATTTTGCGAC 241 AGATTTTGCAAC 303 GACCAAGGTGGAA 301 GACCAAGGTGGA AY062340 M HOMO Sapiens C region mRNN, p	MESSICA ATORISAGUI GIIBBIO/28 KEYWORDS Homo sapiens (human) ORGANISM Homo sapiens Eukaryota, Metazoa; Ch Mammalia; Eutheria; Pr Mammalia; Eutheria; Pr AUTHORS Vaisbourd, M., Ignatovi TITLE Molecular characterizations of tonsila	JOURNAL Unpublished REFERENCE 2 (Dases I to 313) AUTHORS Vaisbourd, M., Ignatovi TITLE Direct Submission JOURNAL Submitted (14-NOV-2001 Road, Cambridge CB2 2Q FEATURES Location/Qual source /organism="Ho /mol type="mm" /db_xref="tax"	/clone=%59/70 /note="amplif" /note="amplif" /locd lymphoc .>313 /codon start= /product="imm region" /protein id="/db_xref="gi: /tdb_xref="gi: /tdb_xref=	ORIGIN Query Match Best Local Similarity 91.7%; Matches 286: Conservative	ATGACCCAGTCTCCATCTT	130	DD 121 CCTAAGCTCCTGATCTATGC QY 190 GGCAGTGGATCTGGGACAGAC
HSA408420 HGA08420 HGGO Saptens partial IGKV gene for immunoglobulin kappa chain variable region, clone 25. AJ408420. GI:1265525 IGKV gene; immunoglobulin kappa chain; immunoglobulin light c variable region. Homo saptens Homo saptens Hokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Mammalia; Eutheria; Primates; Catarthin; Hominidae; Homo. Harfer E., Cooper, S., Neubauer, S., Distel, L. and Grawunder, Universal (1000)	Dreakage syndrome MOL Immunol. 37 (15), 915-929 (2000) 21179652 21179652 2 (bases 1 to 320) Harfst, R. Direct Submission Submitted (04-JAN-2001) Harfst E., Immunologie, Universitaetsklinkum Ulm, Albert-Einstein-Allee 11\$ D-89081 Ulm,	GERMANY Location/Qualifiers 1320 /organism="Homo sapiens" /orlanism="Homo sapiens" /db	/gene="IGKV" 41320 /gene="IGKV" Codon_start=2 /product="immunoglobulin kappa chain variable region" /protoin id="CAC276:14" /db_xref="RBMTREMBL:CAC276:14" /tb_xref="RBMTREMBL:CAC276:14" /translation="IQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQXKPGKAPK LLIYAASTLOSGYPSRSGSGGTBEFILATINBLOPEDPATYYQQLNSYPWTFQGGTK		Similar: 9; Cons	CACTTGCCGGCCCAGTCAGGCCTTAGCTTTTAAATTGGTATCAGGAGCCAGGCAGGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGAGCAGAGAGCAGAGAGCAGAGCAGAGCAGAGCAGAGAGCAGAGAGCAGAGAGCAGAGAGCAGAGACAGAGCAGAGAGCAGAGAGCAGAGAGCAGAGAGACAGAGAGCAGAGAGACAGAGACAGAGACAGAGACAGAGACAGAGAAGA	123 AAAAGCTCCTAAAGCTCCTGATCTATGTTCCATCCAGTTTGCAAAGTGGGGTCCCATCAAG
RESULT 5 H5A408420 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	JOURNAL MEDLINE PUHMED REFERENCE AUTHORS TITLE JOURNAL	FEATURES	ST SCD	V_region ORIGIN	Query Match Best Local Matches 28	6 6 6 7	oy oy oy

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313 bp mRNA linear PRI 23-JAN-2002
9/707 immunoglobulin light chain kappa variable
cds.
                                                                                                                                                                                                                                                                                                                                                                         vich,O., Dremucheva,A., Karpas,A. and Winter,G. sation of human monoclonal antibodies derived il lymphocytes with a human myeloma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ."AAL65713.1"
1.18307284"
MTOSPSSLASASVEDRVTITCRASOSISSYLNWYOOKPGKAPKLL
PSRFSGSOSGTDFTLTISSLQPEDFATYYCQOSYSTSRTFGGGTKVE
CTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ich, O., Dremucheva, A., Karpas, A. and Winter, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11) MRC Laboratory of Molecular Biology, Hills QH, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGC 189
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                                                                                                                                                                                                                                                                                                                        Chordata, Craniata, Vertebrata, Buteleostomi,
Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fied from hybridomas derived from peripheral
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Pred. No. 1.2e-75;
0; Mismatches 26; Indels 0; Gaps
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mmunoglobulin light chain kappa variable
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RNA"
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                                                                                                A 319
                                                             A 321
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nown betations, Chordata, Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 231)
Anderson, E., Henderikx, P., Krambovitis, E., Hoogenboom, H.R. and
Borrebaeck, C.A.K.
A tandem repeat of MUCI core protein induces a weak in vitro immune
response in human B cells
Unpublished
I (bright in the state)
S (bases 1 to 231)
S Anderson, E., Henderikx, P., Krambovitis, E., Hoogenboom, H.R. and
Borrebaeck, C.A.K.
Borrebaeck, C.A.K.
Direct Submission
University, P.O. Box
7031, Lund 220 07, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF090357 321 bp mRNA linear PRI 24-SEP-1998 Homo sapiens clone G8 anti-mucinl light chain variable region mRNA, partial cds.
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                                                  241 AACTIATIACTGTGTACAAGATTACCATGGAGGTTGGCCAAGGGACCAAGGT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AFCACTIGCAGGGCAAGTCAGGACATTAGGTATTTAAATTGGTATCAGCAGAAACCA
181 CAGTGGATCTGGCACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGC
                                  252 GACTIAITACTGTCTAGAGGTTTATAGTACCCTCGGAGGTTCGGCCAAGGGACCTAAGGT
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Best Local Similarity 90.0%; Pred. No. 1.9e-75;
Matches 289; Conservative 0; Mismatches 32; Indels 0;
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AF090357.1 GI:3644021
                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
Homo sapiens
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protein id="AAD16589.1"

/botein id="AAD16589.1"

/db. xref="G1:4323900"

/translation="TGSPSSISASVGBRVTITCRASQGIRNDLGWYQQKPEKAPKLLI
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KRTG"
                                                                                                                                        AF103418 318 bp mRNA linear PRI 03-MAR-1999 Homeo sapiens isolate donor D clone D79K immunoglobulin kappa light chair variable region mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 318)
de Wildt,R.M.T., Hoet,R.M.A., van Venrooij,W.J., Tomlinson,I.M. and
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Winter,d.
Direct Submission
Submitted (29-OCT-1998) Centre for Protein Engineering, MRC, Hills
Road, Cambridge CB2 20H, UK
Road, Cambridge CD2 20H, UK
                                                                                                                                                                                                                                                                                                                                                 Winter, G.
Analysis of heavy and light chain pairings indicates that receptor editing shapes the human antibody repertoire
J. Mol. Biol. 285 (3), 895-901 (1999)
99141150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 GGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGGAAAACCAGGAAAAGCTCC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGCAAGTCAGGGCATTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGAGAAAGCCCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GACCCAGTCTCCATCCTCCCTGTCTGTAGGAGACAGAGTCACCATCACCATGCCG 60
                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 318)
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 GACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACACAGGTCACCATCACTTGCAG
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/codon_start=2
/product="immunoglobulin kappa light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .318
| organism="Nomo sapiens"
| organism="Nomo sapiens"
| faol type="mRNA"
| isolate="donor D"
| db xref="taxon:9606"
| clone="1079x"
| closs="type="peripheral blood"
| fissue type="peripheral blood"
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84.1%; Score 270; DB 9; Length 318;
Best Local Similarity 91.9%; Pred. No. 1.6e-75;
Matches 285; Conservative 0; Mismatches 25; Indels
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Acganism="Homo sapiens"

Advaref="taxon:9606"

Ab xref="taxon:9606"

(cell_type="nRMA"

(cell_type="sbl"|

(cell_t
                                                                                                                                                                                                                                                          HUMVLI 321 bp mRNA linear PRI 17-DEC-2002 Homo sapiens immunoglobulin IgM light chain variable region mRNA, partial cds.
L26035
L26035.1 GI:415710
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                           241 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTGGGACGTTCGGCCAA 300 241 GAAGATTTTGCAACTTATTACTGTCAACAGCTCAATAGTTTCCCCCGGACGTTCGGCCAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AGGTTCAGCGGGGGGACTGGGACGAGGTTCACTCTCACCGTCAGCAGCCTGCAGCCTTAGAGTTCACTCTCACCGTCAGCAGTCTGCAACCTTAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCT
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ilarity 90.0%; Pred. No. 1.9e-75;
Conservative 0; Mismatches 32;
                                                                                                              301 GGGACCAAGGTGGAAATCAAA 321
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Best Local Similarity
Matches 289; Conserv
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AF044451 318 bp mRNA linear SYN 31-0CT-2001 Synthetic construct from Homo sapiens clone IO2 anti-Rh(D) antibody V kappa segment mRNA, partial cds.
AF044451
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Chang, T.Y., Russell, S.L., Bunya, V.Y. and Siegel, D.L.
Direct Submission
Submitted (26-JAN-1998) Path & Lab Med, University of Pennsylvania,
36th & Hamilton, Philadelphia, PA 19104, USA
Location/Qualifiers
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synthetic construct
artificial sequence.

1 (bases 1 to 318)
Siegel, D.L., Chang, T.Y., Russell, S.L. and Bunya, V.Y.
Siegel, D.L., Chang, T.Y., Russell, S.L. and Bunya, V.Y.
solation of cell surface-specific human monoclonal antibodies using phage display and magnetically-activated cell sorting: applications in immunohematology
J. Immunol. Methods 206 (1-2), 73-85 (1997)
97469098
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Chang, T.Y. and Siegel, D.L.
Chang, T.Y. and Siegel, D.L.
Genetic and immunological properties of phage-displayed human
anti-Rh(D) antibodies: implications for Rh(D) epitope topology
Blood 91 (8), 3066-3078 (1998)
98200617
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/db_xref="taxon:32630"
/db_cref="taxon:32630"
/forne_lib="gamma l phage display library R03"
/focus
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84.0%; Score 269.6; DB 12; Length 318;
Best Local Similarity 90.8%; Pred. No. 2.2e-75;
Matches 287; Conservative 0; Mismatches 29; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1...>318
1. .9
/note="pComb3H"
10. .21
/note="VKla primer"
                                                                                             AF044451.1 GI:3046473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 TITIGCAACTIACTACTGTCAACAAGTTACAGTACCCCGTGGACGTTCGGCCAAGGAC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGGAC 305
                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                              Unclassified.

1 (base: 1 to 321)
Siegal.D.E.
Rh(D)-binding proteins and magnetically activated cell sorting method for production thereof Patent: US 6255455-A 218 03-UUL-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      126 AGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified.

1 (base 1 to 321)
Siegla.b.L.
Rh(D)-binding proteins and magnetically activated cell sorting method for production thereof and the production thereof Patent: US 6255455-A 221 03-UL-2001;
Location/Qualifiers
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84.0%; Score 269.6; DB 6; Length
Best Local Similarity 90.8%; Pred. No. 2.2e-75;
Matches 287; Conservative 0; Mismatches 29; Indels
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90.8%; Pred. No. 2.2e-75;
iive 0; Mismatches 29;
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Sequence 221 from patent US 6255455.
AR161049 GI:16226463
Sequence 218 from patent US 6255455.
AR161046
AR161046.1 GI:16226451
                                                                                                                                                                                                            1. 321
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 CAAGGTGGAAATCAAA 321
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Best Local Similarity 90.8<sup>†</sup>
Matches 287; Conservative
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AR161049
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                                                                                                                 CAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGA 245
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   TIGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAAACCAGGGAA 122
                                                                                  182
                                                                                                                                                183 cagrescagresarcressacadarricacreteacearcascagererescaeceas
                                                                                                                                                                                 TTTTGCGACCTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGGAC 305
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                                                   AGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 185
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Siegel, D. 1.
Siegel, D. 1.
Rh(D)-binding proteins and magnetically activated cell sorting method for production thereof
Patent: US 6255455-A 102 03-JUL-2001;
Location/Qualifiers
1 . 321
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT
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Sequence 102 from patent US 6255455.
AR160973.
AR160973.1 GI:16226189
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Matches 287; Conservative
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DNA linear PRI 01-AUG-2001
immunoglobulin kappa chain
                                                                                                            Addoman; amunoglobulin kappa chain; immunoglobulin light chain; IGKV gene; immunoglobulin kappa chain; immunoglobulin light chain; variable region.
Homo sapiens (human)
Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 320)
Harfet, E., Cooper, S., Neubauer, S., Distel, L. and Grawunder, U.
Normal V(D) J recombination in cells from patients with Nijmegen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
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Direct Submission
Submitted (04-JAN-2001) Harfst E., Immunologie,
Universitaetsklinkum Ulm, Albert-Einstein-Allee 11$ D-89081 Ulm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rissue type="peripheral blood lymphocytes (PBL)"
/rearranged
/note="Nijmegen breakage syndrome (NBS) patient"
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/gene="IGKV"
/product="IGKV"
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llarity 90.3%; Pred. No. 2.5e-75;
Conservative 0; Mismatches 31;
                                                                                                                                                                                                                                                                            breakage syndrome
Mol. Immunol. 37 (15), 915-929 (2000)
21179652
                                                                 for
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="22"
                                            320 bp.
Homo sapiens partial IGKV gene f
variable region, clone 22.
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                                                                                                                                 CAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACTCAGCAGCACCTGCAGCCTGAAGA 245
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                                                                       TTGCCGGGCAAGTCAGAGCATTGGCACTTTAAATTGGTATCAGCAGAAACCAGGGAA 122
                                                                                                                   AGCICCIAAGCICCIGAICIAIGIIGCAICCAGIIIGCAAAGIGGGGICCCAICAAGGII 185
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                                                   TTGCAGGGCAAGTCAGGACATTAGGTATTTTAAATTGGTATCAGCAGAAACCAGGAAA 125
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Unkince...
Unclassified.
Unclassified.
I (bases 1 to 321)
Siegel, D.L.
Rh(D)-binding proteins and magnetically activated cell sorting method for production thereof
Patent: US 6259455-A 222 03-UUL-2001;
Location/Qualifiers
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Search completed: June 19, 2004, 05:12:10 Job time : 1846 secs

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June 19, 2004, 03:30:47; Search time 276 Seconds (without alignments) 4940.839 Million cell updates/sec
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GenCore version 5.1.6
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	10111111111111111111111111111111111111	Aah68720 Human ant	Aah68723 Human ant	Aah68647 Human ant	Aah68724 Human ant	Acd45311 Anti-Rh(D	Acd45384 Anti-Rh(D	Acd45388 Anti-Rh(D	Acd45387 Anti-Rh(D	Abz24183 Anti-EGFR	Aah68650 Human ant	Acd45314 Anti-Rh(D	Aav19759 Antibody	Aba06023 Human mon	Aah68718 Human ant	N	Acd45382 Anti-Rh(D	Acd45316 Anti-Rh(D	Aah68649 Human ant	Aah68643 Human ant	Aah68709 Human ant	۲.	Acd45313 Anti-Rh(D	Acd45373 Anti-Rh(D
SUMMARIES	TD .		AAH68720	AAH68723	AAH68647	AAH68724	ACD45311	ACD45384	ACD45388	ACD45387	ABZ24183	AAH68650	ACD45314	AAV19759	ABA06023	AAH68718	AAH68652	ACD45382	ACD45316	AAH68649	AAH68643	AAH68709	ACD45307	ACD45313	ACD45373
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Aat66781 Anti-canc	Abs52471 Human DNA	Aav19743 Antibody	Aah47731 Nucleotid	Aah47735 Nucleotid	Aah68717 Human ant	Aah68719 Human ant	Aah68703 Human ant	Acd45367 Anti-Rh(D	Acd45383 Anti-Rh(D	Acd45381 Anti-Rh(D	Aav19757 Antibody	Aav19761 Antibody	Aal45699 Human end	Aba94337 MAb 63 li	Aah68713 Human ant	Acd45377 Anti-Rh(D	Aav19745 Antibody	Aah68654 Human ant	Aah68701 Human ant	Acd45318 Anti-Rh(D	Acd45365 Anti-Rh(D
AAT66781	ABS52471	AAV19743	AAH47731	AAH47735	AAH68717	AAH68719	AAH68703	ACD45367	ACD45383	ACD45381	AAV19757	AAV19761	AAL45699	ABA94337	AAH68713	ACD45377	AAV19745	AAH68654	AAH68701	ACD45318	ACD45365
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82.3	82.1	81.6	81.6	81.6	81.5	81.5	81.5	81.5	81.5	81.5	81.1	81.1	81.1	81.1	81.0	81.0	80.5	80.5	80.5	80.5	80.5
263.4	263.4	261.8	261.8	261.8	261.6	261.6	261.6	261.6	261.6	261.6	260.2	260.2	260.2	260.2	260	260	258.4	258.4	258.4	258.4	258.4
24	25	56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	4. rv

ALIGNMENTS

RESULT 1

Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant; red blood cell; Rh phenotype; diagnosis; therapeutic; ds. New isolated protein, preferably a human anti-Rh(D) antibody for ue diagnostics requiring a human instead of an animal antibody and in therapeutic medicine. Human anti-Rh(D) antibody clone SH49 nucleotide sequence. BP. 96US-0028550P. 97US-00884045. 98US-0081380P. 99US-00240274. AAH68720 standard; DNA; 321 (first entry) (UYPE-) UNIV PENNSYLVANIA. WPI; 2001-388931/41. P-PSDB; AAG93663. US6255455-B1. 14-SEP-2001 Homo sapiens 03-JUL-2001. 29-JAN-1999; 11-OCT-1996; 27-JUN-1997; 10-APR-1998; Siegel DL; AAH68720; AAH68720

Example 3; Col 79; 162pp; English.

use in

The present invention describes an isolated Rh(D) binding protein, one ferably a human antibody, (I) having an amino acid sequence comprising one of the sequences (S) given in AAG93558 to AAG93669. (I) has immunostimulant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostics that require human antibodies intagnostics that require human antibodies autibodies, such as determine the Rh phenotype of human red blood cells. AAH68615 to AAH68726 represent the nucleotide sequence which encode

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Length 321; Indels 65 62 125 122 185 182 245

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The present invention describes an isolated Rh(D) binding protein, preferably a human antibody, (I) having an amino acid sequence comprising one of the sequence comprising one of the sequence (S) given in hAG93558 to AAG93669. (I) has immunostimulant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAG93558 to AAG93670 to AAG93697 represent anti-Rh(D) heavy chain CDR3 amino acid sequences which are given in the exemplification of
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123 AGCCCTAAGGTCCTGATCTATGCTGCATCAGTTTGCAAAGTGGGGTCCCATCAAGGTT
123 AGCCCTAAGGTCCTGATCTATGCTGCATCAGTTTGCAAAGTGGGGTCCCATCAAGGTT
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red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
                                                                                                                                                                  Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                             84.0%; Score 269.6; DB 5; 90.8%; Pred. No. 1.1e-78; tive 0; Mismatches 29;
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Best Local Similarity 90.8
Matches 287; Conservative
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                                                                                                                                         the present invention
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27-JUN-1997;
10-APR-1998;
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  AAG93558 to AAG93669, AAG93670 to AAG93697 represent anti-Rh(D) heavy chain CDR3 amino acid sequences which are given in the exemplification of the present invention
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                                                                                                                                          6 CCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCAC
                                                                                                                                                           CAAGCTCACCCAGTCTCCCTGTCTGTCTGTTGTAGGAGACAGAGTCACCGTCAC
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                                                                               Query Match 84.0%; Score 269.6; DB 5; Length 321; Best Local Similarity 90.8%; Pred. No. 1.1e-78; Matches 287; Conservative 0; Mismatches 29; Indels 0.
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                                                        Seguence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;
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                                                                                       The present invention describes an isolated Rh(D) binding protein, preferably a human antibody. (I) having an amino acid sequence comprising one of the sequences (S) given in AAG93558 to AAG93669. (I) has immunostimmlant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostic that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood calls. AAEG8615 to AAH68726 represent the nucleotide sequence which encode thain CDR3 amino acid sequences which are given in the exemplification of the present invention
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                    New isolated protein, preferably a human anti-Rh(D) antibody for use in diagnostics requiring a human instead of an animal antibody and in therapeutic medicine.
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red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
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84.0%; Score 269.6; DB 5; Length 321;
Best Local Similarity 90.8%; Pred. No. 1.1e-78;
Matches 287; Conservative 0; Mismatches 29; Indels 0.
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                                                                                                                                                                                                                                         Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
                                                                      Example 2; Col 54; 162pp; English
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The present invention describes an isolated Rh(D) binding protein, preferably a human antibody, (I) having an amino acid sequence comprising one of the sequences (S) given in AAG93586 to AAG93589. (I) has intermedetimulant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAH68615 to AAH68726 represent the nucleotide sequence which encode hado3558 to AAG93670 to AAG93697 represent anti-Rh(D) heavy chain CDR3 amino acid sequences which are given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITIGGGACTIATEACIGICTACAGGITTAFAGIACCCCTCGGACGTTCGGCCAAGGGAC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                            preferably a human anti-Rh(D) antibody for use in a human instead of an animal antibody and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 TTTGCAACTTACTACTGTCAACAGAGTTACAGTACCGGGGGAGGGTCGGGCCAAGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 CGAGCTCACCCCAGTCTCCATCCTCCATGTCTGCATCTGTAGGAGACAGAGAGTCACCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 TIGCAGGCAAGICAGGACATTAGGTATTAATTTAGGTATCAGCAGAAACCAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 CCACATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCGGCCTGCAGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ds; gene; RH(D) binding protein; blood typing; blood product;
magnetically activated cell sorting.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

84.0%; Score 269.6; DB 5; Length

Best Local Similarity 90.8%; Pred. No. 1.1e-78;

Matches 287; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                     Example 3; Col 80; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGGTGGAAATCAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGGTGGAAATCAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACD45311 standard; DNA; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                             (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-Rh(D) chain 102 DNA
                                                                                                                                                                                                              New isolated protein,
diagnostics requiring
therapeutic medicine.
                                                                                                                                                WPI; 2001-388931/41.
                                                                                                                                                                       P-PSDB; AAG93667.
27-JUN-1997;
10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-2003
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                                                                                                         Siegel DL;
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96US-0028550P. 97US-00884045. 98US-0081380P. 99US-00240274.

2001US-00848798

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(UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                      WPI; 2003-512273/48.
P-PSDB; ABO27470.
                           US2003040605-A1
                                                                                  11-OCT-1996;
27-JUN-1997;
10-APR-1998;
29-JAN-1999;
                                                                04-MAY-2001;
          Homo sapiens
                                              27-FEB-2003
                                                                                                                                                   Siegel DL;
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                                                                                                                                                                                                                                                                                                                                                                                                                         126 AGCTCCTAAGCTCCTGATCTATGTTGCATCTAGCAAGTGGGGTCCCATCAAGGTT 185
123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGGTCCCATCAAGGTT 182
                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                              The invention relates to an isolated Rh(D) binding protein. The protein can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents DNA encoding a human anti-Rh(D) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 CAGTGGCAGTGTGGATCTGGGACAGTTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA
                                                                                                                                                                                                                                                                                                                                                 CCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACCAGAGTCACCATCAC
                                                                                                                                                                                                                                                                                                                                                           CACCOCCAGACACACAGACTCCACTCACCGTCACCAGCCTGCAGCCTGAAGA
                                                                                                                                                                                 New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products.
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, ds., gene, RH(D) binding protein; blood typing, blood product,
magnetically activated cell sorting.
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                                                                                                                                                                                                                                                                                                           DB 8; Length 321;
                                                                                                                                                                                                                                                                                                          Query Match
84.0%; Score 269.6; DB 8; Length
Best Local Similarity 90.8%; Pred. No. 1.1e-78;
Matches 287; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                        Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                              Claim 12; Page 39; 187pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-Rh(D) light chain SH49 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0028550P.
97US-00884045.
98US-0081380P.
99US-00240274.
                                               2001US-00848798
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                                                                                                                 (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                     WPI; 2003-512273/48.
P-PSDB; ABO27397.
          US2003040605-A1
                                               04-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2003
                                                                  11-0CT-1996;
27-JUN-1997;
                                                                                    10-APR-1998;
29-JAN-1999;
                            27-FEB-2003
                                                                                                                                    Siegel DL;
                                                                                                                                                                                                                                                                                                                                                                                       99
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                                                                                                                                                                                                                                                                                                                                                                      63 TIGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGGAGAAACCAGGGAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TETTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGGAC 305
                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                  62
                                                                              The invention relates to an isolated Rh(D) binding protein. The protein can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents DNA encoding a human anti-Rh(D) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCGGCAGTGGATCTGGGACAGAGTTCACCCTCACCGCTCACCAGCCTGAAGA
                                                                                                                                                                                                                                                                                  TIGCAGGGCAAGTCAGGACATTAGGTATTAAATTGGTATCAGCAGAAACCAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                      New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products.
                                                                                                                                                                                                                                                                                                                                                                                                                      ACCICCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGGTCCCATCAAGGTT
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                               84.0%; Score 269.6; DB 8; Length 321; 90.8%; Pred. No. 1.1e-78; Artive 0; Mismatches 29; Indels 0;
                                                                                                                                                                                    Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;
                                                      Claim 12; Page 61; 187pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGGTGGAAATCAAA 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 321
                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.8
Matches 287; Conservative
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ID ACD4
XX ACD4
XC ACD4
XX DT 12-8
XX DE Anti
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The invention relates to an isolated Rh(D) binding protein. The protein can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents DNA encoding a human anti-Rh(D) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITIGGACTIVITACIGICIACAGGITIVATAGIACCCCICGGACGITICGGCCAAGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTGCAACTTACTACTGTCAACAGAGTFACAGTACCCCGTGGACGTTCGGCCAAGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CGAGCTCACCCCAGTCTCCCCATGTCTGCATCTGTAGGAGACAGAGTCACCATCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGCAGGGCAAGICAGGACATIAGGIAITAATITAAATIGGTATCAGCAGAAACCAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCAC
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                             product;
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84.0%; Score 269.6; DB 8; Length 321;
Best Local Similarity 90.8%; Pred. No. 1.1e-78;
Matches 287; Conservative 0; Mismatches 29; Indels 0;
                            binding protein; blood typing; blood cell sorting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 61; 187pp; English.
  DNA
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97US-00884045.
98US-0081380P.
99US-00240274.
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                                                                                                                                                      2001US-00848798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321
Anti-Rh(D) light chain SH52
                                                                                                                                                                                                                                                   UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; cDNA;
                          Human; ds; gene; RH(D) magnetically activated
                                                                                                                                                                                                                                                                                                          WPI; 2003-512273/48.
P-PSDB; ABO27473.
                                                                                               US2003040605-A1.
                                                                                                                                                                               11-OCT-1996;
27-JUN-1997;
10-APR-1998;
                                                                                                                                                     04-MAY-2001;
                                                                     sapiens
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                                                                                                                          27-PEB-2003
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                                                                                                                                                                                                                                                                               Siegel
                                                                      Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGGAC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
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                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated Rh(D) binding protein. The protein can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents DNA encoding a human anti-Rh(D) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGCTCACCCAGTCTCCATCCTCCATGTCTGCATCTGTAGGAGACAGAGTCACCATCAC
                                                                                                                                                                                                                                                                                                                      various diagnostic and of blood or blood products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGATGACCCAGTCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACGGTCAGCAGCCTGCAGCCTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  typing; blood product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.8%; Pred. No. 1.1e-78;
Matches 287; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
 Human, ds; gene, RH(D) binding protein, blood magnetically activated cell sorting.
                                                                                                                                                                                                                                                                                                                      New human Rh(D)-binding protein useful for therapeutic applications, including typing
                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 61; 187pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР.
                                                                                                                                                   96US-0028550P.
97US-00884045.
98US-0081380P.
99US-00240274.
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                                                                                                                          2001US-00848798
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                                                                                                                                                                                                                         (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                            WPI; 2003-512273/48.
P-PSDB; ABO27474.
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                                                                   US2003040605-A1.
                                                                                                                                                     11-OCT-1996;
27-JUN-1997;
16-APR-1998;
29-JAN-1999;
                                          Homo sapiens
                                                                                                                          04-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2003
                                                                                               27-FEB-2003
                                                                                                                                                                                                                                                   Siegel DL;
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Novel isolated human monoclonal antibody which binds to human epidermal growth factor receptor, useful for treating or preventing a disease mediated by expression of epidermal growth factor receptor such as
                                   Monoclonal antibody, MAb, 2F8, human, epidermal growth factor receptor, EGFR; immunoglobulin; cytostatic; immunosuppressive; antiinflammatory; antiarthritic, antipsoriatic; gene; ds.
                                                                                        Location/Qualifiers
1. .321
/*tag
/*tag
/product= "VL chain"
/product= "the start and stop codons are not indicated"
                                                                                                                                                                                                                                                        Dijk MA, Gerritsen AF, Halk E;
                 Anti-EGFR antibody 2F8 VL chain encoding DNA
                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 15A; 117pp; English.
                                                                                                                                                                                       13-JUN-2002; 2002WO-US018748.
                                                                                                                                                                                                          13-JUN-2001; 2001US-0298172P.
(first entry)
                                                                                                                                                                                                                                                        Van De Winkel J, Van
                                                                                                                                                                                                                           (GENM-) GENMAB AS. (MEDA-) MEDAREX INC.
                                                                                                                                                                                                                                                                          WPI; 2003-167368/16.
P-PSDB; ABB82945.
                                                                                                                                                  WO2002100348-A2
                                                                         Homo sapiens
14-APR-2003
                                                                                                                                                                     19-DEC-2002
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which binds to human epidermal growth factor receptor (ECFR), where the Mab is selected from immunoglobulin (1g)GJ, 1gA, 1gE, 1gM, 1gG4 and 1gD antibodies. The Mab is useful for inhibiting growth of a cell expressing cFRR, for inducing cytolysis of a cell expressing ECFR, or for detecting the presence of EGFR antigen, or a cell expressing ECFR. It is useful for realing or preventing a disease mediated by expression of EGFR, the disease is cancer (such as bladder, breast, colon, kidney, ovarian, prostate, renal, or head and neck cancer), or an autoimmune disease (such as inflammancy arthritis), where the autoimmune disease involves opithelial hyperproliferation. The Mab can be conjugated to a binding specificity for a FC receptor or to a cytocoxin. It is useful as diseases, for inhibiting growth and/or mediating phagocytosis and killing of cells expressing EGFR, for treating autoimmune disease such as psecificity for a cell expressing EGFR, to mediating phagocytosis or cytolysis of a cell expressing EGFR, to resample for labeling colls, to inhibit EGF or TGF-alpha induced autophosphorylation of EGFR, to target cells expressing FGFR in the presence of human effector cells, to inhibit EGF or TGF-alpha induced autophosphorylation of EGFR, to target cells expressing regiment or EGFR, for example for labeling such an orled on the UL chain of an anti-EGFR antibody 2F8 and the EGFR expresents invention relates to an isolated human monoclonal antibody (MAb)

Sequence 321 BP; 81 A; 85 C; 77 G; 78 T; 0 U; 0 Other;

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                                                                                                           1 GACATCCAGATGACCCCAGTCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 60
  DB 7; Length 321;
Query Match

83.6%; Score 268.2; DB 7; Length
Best Local Similarity 89.7%; Pred. No. 3.3e-78;
Matches 288; Conservative 0; Mismatches 33; Indels
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ATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCA 120 61

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Length 321;

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268;

Score

83.58;

Query Match

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The present invention describes an isolated Rh(D) binding protein, preferably a human antibody, (I) having an anino acid sequence comprising one of the sequences (S) given in AAG93558 to AAG93669. (I) has immunostimulant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAG93558 to AAG93679, to AAG93679 represent which encode AAG93679 amino acid sequences which are given in the exemplification of
                                                                                            240
                                                                                                                     240
300
                                                                                                                                                GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preferably a human anti-Rh(D) antibody for use in a human instead of an animal antibody and in
                                        AGGTTCAGCGGCAGTGAATCTGGGGACAGATTTCAGTCTCACCATCAGCAGCCTGCAGCCT
                                                                                                                                                                 GAAGATTTTGCAACTTATTACTGTCAACAGTTTAAATAGTTACCCGCTCACTTTGGGGGA
                                                                                            AGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCACCGTCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                      Human; anti-Rh(D) antibody, Rh(D) binding protein; immunostimulant;
red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 321 BP; 87 A; 88 C; 73 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                               Human anti-Rh(D) chain IO5 nucleotide seguence.
                                                                                                                                                                                                     GGGACCAAGGTGGAAATCAAA 321
                                                                                                                                                                                                                              GGGACCAAGGTGGAGATCAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Col 55; 162pp; English
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97US-00884045.
98US-0081380P.
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                                                                                                                                                                                                                                                                                                  AAH68650 standard; DNA; 321
                                                                                                                                                                                                                                                                                                                                                    14-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated protein,
diagnostics requiring
therapeutic medicine.
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P-PSDB; AAG93593.
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27-JUN-1997;
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Length 321;

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Query Match
83.5%; Score 268; DB 8;
Best Local Similarity 90.5%; Pred. No. 3.9e-78;
Matches 286; Conservative 0; Mismatches 30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGGTGGAAATCAAA
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P-PSDB; AAW52235.
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                                                                                                                                                                                                                      246 TTTIGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGGAC 305 243 TTTTGCAACTTACTACTGTCAACAGGTTACAGTACCCCTCAAACGTTCGGCCAAGGGAC 302
                                                                                                                                           125
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                                                                                                                                           CACTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGCAACCTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              various diagnostic and of blood or blood products
                                                                                                                                                                                                                                                                                                          CAGCGGCAGTGGGATCTGGGACAGATTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGA
                                                                CCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCAGGGGACAGAGTCACCATCAC
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated Rh(D) binding protein. The prot can be used for magnetically activated cell sorting. The protein is useful in various diagnostic and therapeutic applications in humans, including typing of blood or blood products. The present sequence represents DNA encoding a human anti-Rh(D) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ds, gene, RH(D) binding protein; blood typing, blood product,
magnetically activated cell sorting.
                         .;
    Pred. No. 3.9e-78;
0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human Rh(D)-binding protein useful for therapeutic applications, including typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 40; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 321 BP; 87 A; 88 C; 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0028550P.
97US-00884045.
98US-0081380P.
99US-00240274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGGTGGAAATCAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGGTGGAAATCAAA 321
90.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYPE-) UNIV PENNSYLVANIA
Best Local Similarity 90.53
Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-Rh(D) chain 105 DNA
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P-PSDB; ABO27400.
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27-JUN-1997;
10-APR-1998;
29-JAN-1999;
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                                                                           125
                                                                                                      122
                                                                                                                                 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Rhesus D antigen binding poly:peptide(s) - used to neutralise Rhesus D antigen in therapy, e.g. for treating idiopathic thrombocytopenic purpura.
                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes the antibody LD2-17-VL chain sequence, which is a polypeptide of the invention. The polypeptides are capable of forming antigen binding structures with specificity for Rhesus D antigens which include Rhesus D-specific Nr. 2, and CDR 3 regions of pairs of variable heavy (VH) and variable light (VL) chain sequences. The
                                                                                                                                                                                    126 AGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT
123 AGCCCCTAAGCTCCTGATCTTTGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT
                                    3 CARGETCACCCCAGTCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC
                                                                           TTGCAGGGCAAGTCAGGACATTAGGTATTTTAAATTGGTATCAGCAGAAACCAGGAAA
                                                                                            CCAGATGACCCCAGTCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCAC
 Gaps
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 30; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ROTK-) ROTKREUZSTIPTUNG ZENT LAB BLUTSPENDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody LD2-17-VL chain coding sequence.
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08-MAY-2001; 2001WO-US015114 08-MAY-2000; 2000US-0203126P.

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antibodies are active against the Rhesus D antigen. They can be used for treating disorders which would benefit from anti-Rhesus D immunoglobulin, e.g. idiopathic thrombocytopenic purpura. They can also be used for the protection of Rhesus negative women before or immediately after the bitth of a Rhesus positive child to prevent haemolytic disease of the newborn (fMDN) in subsequent pregnancies. In addition, anti-Rhesus D immunoglobulin can be used after mistransfusions of Rhesus positive blood to Rhesus negative recipients in order to prevent sensitisation to the Rhesus D antigen. The products can also be used as diagnostic reagents
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                                                                                                                                                                                                                                                                                                                        CAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAAGC 128
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                                                                                                                                                                                                                                                                                                                                                                                        TCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAG 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGACCCAGTCTCCCATCTTCCCTGTCTGCTAGGGGACAGAGTCACCATCACTTG
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                             DB 2; Length 315;
                                                                                                                                                                                            / Match B3.1%; Score 266.6; DB 2; Length Dcoal Similarity 90.7%; Pred. No. 1.1e-77; Length Bs 284; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                  Sequence 315 BP; 80 A; 82 C; 77 G; 76 T; 0 U; 0 Other;
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New human monoclonal antibodies specific for dendritic cells, useful for inhibiting growth or inducing cytolysis of a dendritic cell and treating or preventing a dendritic cell mediated disease, e.g., autoimmune

WPI; 2002-089788/12.

Deo YM,

P-PSDB; AAM48004

(MEDA-) MEDAREX INC Keler T; Example 2; Fig 13; 95pp; English

disorders

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Human, monoclonal antibody, B11; antigen binding portion; dendritic mannose receptor; growth, cytolysis; pathogen, virus; bacterium; autoimmune disease; inflammatory disorder; rheumatoid arthritis; multiple solerosis, diabetes melliture; immunomodulatory; antiinflammatory; antiarthritic; neuroprotective; antidiabetic, antianaemic; endocrine; dermatological; antithyroid; uropathic; ophthalmological; muscular; gene; ds.
                                                                         Human monoclonal antibody B11 variable light chain DNA.
                                                                                                                                                                                                                                 Location/Qualifiers
멾
 ABA06023 standard; DNA; 321
                                                  (first entry)
                                                                                                                                                                                                        Homo sapiens
                                                   08-MAR-2002
                         ABA06023
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1. .321
/*tag= a
/product= "Human monoclonal antibody B11 variable light
chain"
/partial
/note= "CDS lacks an initiation codon and a stop codon"

WO200185798-A2

15-NOV-2001

cell;

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The invention relates to human monoclonal antibodies or their antigen

binding portions that specifically bind to dendritic cells and has one or

competed the following characteristics: (a) a binding affinity constant to

a dendritic cell of at least about 10 to the power 7 M-1; (b) the ability constant to

compense a dendritic cell; (c) the ability to internalise after

to opsonise a dendritic cell; (c) the ability to internalise after

colls. The isolated human monoclonal antibody or its antigen binding

colls. The isolated human monoclonal antibody or its antigen binding

colls. The allowing colls; in the presence of human effector cells; or

cytolysis of dendritic cells. The antibodies or its antigen

complete in thibitic cells in the presence of human manose receptor on

binding portion, binds to and blocks the human manose receptor on

complete in thibitic cells. The antibodies or its antigen

complete in the antibodies have immunomodulatory, antiinflammatory,

antirheumatic, antiarthitic, neuroprotective, antidabetic, antianaemic,

antirheumatic, antiarthiting growth of a dendritic cell, inducing cytolysis of

dendritic cell, treating or preventing a dendritic cell, inducing cytolysis of

dendritic cell and preventing binding of a pathogen (a virus or a

confercing the presence of a dendritic cell, inducing cytolysis of

dendritic cell and preventing binding of a pathogen (a virus or a

confercing in mannose receptor on dendritic cells. In particular,

the antibodies may be used to treat, autoimmune disease, graft versus

confercing anaemia, Addison's disease, lupus erythematosus, Reiter's

conforme and Graves disease. The present sequence is that of the human

conforme and Graves disease. The present sequence is that of the human

conformed antibody Bll variable light chain, useful to the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTTCAGCGGCAGTGGGATCTGGGACTTCACTCTCACCGTCAGCAGCCTGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACATCCAGATGACCCCAGTCTCCCATCTTCCCTGTCTGCAGGGGACAGAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 321 BP; 84 A; 84 C; 80 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 266.6; DB 6
Pred. No. 1.1e-77;
0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGACCAAGGTGGAAATCAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.1%;
89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.4
Matches 287; Conservative
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The present invention describes an isolated Rh(D) binding protein, preferably a human antibody, (I) having an amino acid sequence comprising one of the sequences (S) given in AAG93558 to AAG93669. (I) has immunostimulant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAH68615 to AAH68726 represent the nucleotide sequence which encode AAG93569. AAG93690 to AAG93697 represent anti-Rh(D) heavy chain CDB3 manno acid sequences which are given in the exemplification of
CAGTGGCAGTGGATCTGGGAAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242
                                                                        243 TITIGEAACTACTACTACTGTGAACTACAGTTATCCTGGCAAGGGAG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 TIGCAGGGCAAGICAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated protein, preferably a human anti-Rh(D) antibody for use in diagnostics requiring a human instead of an animal antibody and in therapeutic medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 ccagargacccagrerecarerrecersrerecareragagacagacaccareae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                          ) antibody; Rh(D) binding protein; immunostimulant; Rh phenotype; diagnosis; therapeutic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.0%; Score 266.4; DB 5; Length 321; 90.2%; Pred. No. 1.3e-77; ive 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 321 BP; 85 A; 87 C; 76 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                              Human anti-Rh(D) chain I07 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3xample 2; Col 55; 162pp; English.
                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0028550P.
97US-00884045.
98US-0081380P.
                                                                                                                                                   303 CAAGGTCGAGATCAGA 318
                                                                                                                     306 CAAGGTGGAAATCAAA 321
                                                                                                                                                                                                                                 AAH68652 standard; DNA; 321
                                                                                                                                                                                                                                                                                                   (first entry)
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285; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-388931/41.
                                                                                                                                                                                                                                                                                                                                                                 anti-Rh(D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAG93595
                                                                                                                                                                                                                                                                                                                                                                   Human; anti-Rh(D
red blood cell;
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6255455-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUN-1997;
10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-0CT-1996;
                                                                                                                                                                                                                                                                                                   14-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Siegel DL;
                                                       246
                        183
                                                                                                                                                                                                                                                                  AAH68652;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an isolated Rh(D) binding protein, preferably a human antibody. (I) having an amino acid sequence comprising one of the sequence comprising immunostimmlant activity, and can be used as an immune system stimulant. (I) can be used in diagnostic and therapeutic medicine. The antibodies are used in diagnostics and therapeutic medicine. The antibodies are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAKi66615 to AAK69726 represent the nucleotide sequence which encode AAK931670 to AAA93497 represent anti-Rh(D) heavy chain CDR3 amino acid sequences which are given in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 TEGCAGGGCAAGTCAGGACATTAGGTATTAAATTGGTATCAGCAGAAACCAGGAAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEGCCGGGCAAGTCAGAGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGAAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 AGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated protein, preferably a human anti-Rh(D) antibody for use diagnostics requiring a human instead of an animal antibody and in therapeutic medicine.
                                                                                                                                                                                                                                  n, anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant; blood cell; Rh phenotype; diagnosis; therapeutic; ds.
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                                                                                                                                                                                                     Human anti-Rh(D) antibody clone SH47 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 321 BP; 86 A; 88 C; 73 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.0%; Score 266.4; DB 5
90.2%; Pred. No. 1.3e-77;
iive 0; Mismatches 31
      301 GGGACCAAGGIGGAAATCAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Col 78; 162pp; English.
                                                                                                         AAH68718 standard; DNA; 321 BP
                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0028550P.
97US-00884045.
98US-0081380P.
                                                                                                                                                                                                                                                                                                                                                                                      99US-00240274
                                                                                                                                                                        14-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 285; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAG93661.
                                                                                                                                                                                                                                                                                                                      US6255455-B1.
                                                                                                                                                                                                                                                                                      Homo sapiens.
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205, App 206, App 200, App 213, App 213, App 36, App 36, App 114, App 114, App 208, App 72, App 76, App

Sequence Sequence

US-09-240-274-105
US-09-240-274-106
US-09-240-274-103
US-09-240-274-103
US-08-599-26-36
US-09-125-098-36
US-09-540-274-104
US-09-540-274-104
US-09-540-274-108
US-09-540-274-208
US-08-488-113B-72
US-08-488-113B-72
US-08-477-4848-75
US-08-477-788-75
US-08-488-75
US-08-477-788-75
US-08-477-788-75

13

Run

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TYPE: DNA
ORGANISM: Homo sapiens
RESULT 1
US-09-240-274-102
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Sequence 107, App
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Sequence 12, Appl
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TITLE OF INVENTION: RA(D)-BINDING PROTEINS AND MAGNETICALIX ACTIVATED CELL
TITLE OF INVENTION: RA(D)-BINDING POR PRODUCTION THEREOF
TITLE REPERRENCE: 09596-4402
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-04-10
EARLIER PILING DATE: 1999-04-10
EARLIER PILING DATE: 1999-04-10
EARLIER PILING DATE: 1999-04-10
EARLIER PILING DATE: 1996-10-11
NUMBER: OF SEQ ID NOS: 224
SOFTWARE: PALENT VELL VET: 2.0
SEQ ID NO 102
LENGTH: 321
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ALIGNMENTS
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                                                                                                    ; Sequence 102, Application US/09240274; Patent No. 6255455; GENERAL INFORMATION:
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Matches 287; Conservative
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Best Local Similarity 90.8%;
Matches 287; Conservative
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SEQ ID NO 222
LENGTH: 321
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Best Local Similarity 90.8
Matches 287; Conservative
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 221
LENGTH: 321
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ORGANISM: Homo sapiens
FEATURE:
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Patent NO. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REPERENCE: 09596-4210.
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
BARLIER PILING DATE: 1999-01-29
BARLIER PILING DATE: 1998-04-10
BARLIER APPLICATION NUMBER: 60/028,550
BARLIER FILING DATE: 1996-10-11
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84.0%; Score 269.6; DB 3; Length 321;
Best Local Similarity 90.8%; Pred. No. 4.9e-81;
Matches 287; Conservative 0; Mismatches 29; Indels 0
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US-09-240-274-218
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ORGANISM: Homo sapiens
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APPLICANT: Siegel, Donald L.
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: CORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT PRILING DATE: 1999-01-29
CURRENT PILING DATE: 1999-01-29
EARLIER FILING DATE: 1999-04-10
EARLIER FILING DATE: 1996-04-10
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
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                                                                                                                      Score 269.6; DB 3;
Pred. No. 4.9e-81;
0; Mismatches 29;
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US-09-240-274-222
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-221
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90.8%; Pred. No. 4.9e-81;
tive 0; Mismatches 23
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TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 105, Application US/09240274

JETER No. 6255455

GENERAL INFORMATION:
JAPLICANT: Siegel, Donald i.
JITLE OF INVENTION: RATHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

JUREARY PRILING DATE: 1999-01-29

BARLIER FILING DATE: 1998-01-10

BARLIER FILING DATE: 1998-01-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 105

LENGTH: 321
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243 TITIGCAACTFACTACTGCCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGAC 302
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US-09-240-274-105
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ORGANISM: Homo sapiens
FEATURE:
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US-09-240-274-216
US-09-240-274-216
Sequence 216, Application US/09240274
Sequence 216, Application US/09240274
Sequence 216, Application US/09240274
Sequence 216, Application US/09240274
Sequence 1 INFORMATION:
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: Rh(D)-BINDING PROPUCTION THEREOF
TITLE OF INVENTION: NUMBER: US/09/240, 274
CURRENT FILING DATE: 1999-01-29
CURRENT FILING DATE: 1999-01-29
SEARLIER APPLICATION NUMBER: 60/028,550
RARLIER APPLICATION NUMBER: 60/028,550
RARLIER PILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 216
WS-09-274-107

Sequence 107, Application US/09240274

Sequence 107, Application US/09240274

Sequence 107, Application US/09240274

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Sh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SN(D)-202

CURRENT APPLICATION WHORER: US/09/240,274

CURRENT PILING DATE: 1999-01-29

SARLIER APPLICATION NUMBER: 60/081,380

RARLIER PILING DATE: 1998-04-10

RARLIER PILING DATE: 1998-04-10

SARLIER PILING DATE: 1998-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PATENTIN Ver. 2.0

SEQ OFTWARE: PATENTIN Ver. 2.0
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83.0%; Score 266.4; DB 3; Length
Best Local Similarity 90.2%; Pred. No. 5.9e-80;
Matches 285; Conservative 0; Mismatches 31; Indels
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; OTHER INFORMATION: anti-Rh(D) chain 107
US-09-240-274-107
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126 AGCTCCTAAGCTCCTGATCTATGTTGCATTTGCAAAGTGGGGTCCCATCAAGGTT 185
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243 TICIGCAACTIAITACTGTCTACAGCATAATAGTTTCCCGTGGACGTTCGGCCAAGGGAC 302
AGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 185
                 123 AGCCCTAAGGTCCTGAICTATGCTGCATCTGCAAAGTGGGGTCCCATCAAGGTT
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Pred. No. 2e-79;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
PRATURE:
OTHER INFORMATION: anti-Rh(D) chain 104
US-09-240-274-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGGTGGAAATCAAA 318
                                                                                                                                                             CAAGGTGGAAATCAAA 321
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Best Local Similarity 89.9%;
Matches 284; Conservative 0
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US-09-240-274-207
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US-09-240-274-98

J Sequence 98, Application US/09240274

Sequence 98, Application US/09240274

REQUENCE 98, Application US/09240274

SEQUENCE 98, Application US/09240274

GENERAL INFORMATION:

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: 1996-4202

CURRENT APPLICATION NUMBER: 06/081,380

BARLIER APPLICATION NUMBER: 06/081,380

BARLIER APPLICATION NUMBER: 60/081,380

BARLIER PILLING DATE: 1996-04-10

BARLIER FILLING DATE: 1996-01-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 98

LENGTH: 321

TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                            242
                                                                                                                                                                                                                                                                                                                                                                    246 TITIGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGGAC 305
243 TITIGCAACTTACTACTGTCAACAGAGTTACAGTTATCCTCGCAAGGCAAGGGAC 302
                                                                                                                                                                                                       TTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAA 125
                                                                                                                                                                                                                                                                                                                   CAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGAAGA 245
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                                                                                                                                                      6 CCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTAGGGGACAGAGTCACCATCAC
                                                                                                                                                                    3 CGAGCTCACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGACACCATCAC
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                                                                                               Length 321;
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                                                                                               Query Match 83.0%; Score 266.4; DB 3; Length Best Local Similarity 90.2%; Pred. No. 5.9e-80; Matches 285; Conservative 0; Mismatches 31; Indels
                     ; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: anti-Rh(D) antibody clone SH47

US-09-240-274-216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: anti-Rh(D) chain F01
US-09-240-274-98
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FEATURE:
        LENGTH: 321
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REPERENCE: 09596-4212
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT APPLICATION NUMBER: US/09/240,274
EARLIER APPLICATION NUMBER: 60/081,380
BARLIER PILING DATE: 1998-04-10
BARLIER FILING DATE: 1998-04-10
BARLIER FILING DATE: 1996-04-10
BARLIER FILING DATE: 1996-04-10
BARLIER FILING NUMBER: 60/028,550
BARLIER FILING NUMBER: 60/028,550
BARLIER FILING NOS: 224
SOFTWARE: PATENTING NOS: 224
SOFTWARE: PATENTING NOS: 224
SOFTWARE: 200
BARLIER FILING DATE: 1996-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 TIGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 AGCTCCTAAGCTCCTGATCTATGTTGCAAGTTTGCAAAGTGGGGTCCCATCAAGGTT 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 TTTTGCAACTTACTACTGTCAACAGAGTTCCAGTACCCCGTGGACGTTCGGCCGAGGGAC 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.5%; Score 264.8; DB 3; Length 321; 89.9%; Pred. No. 2e-79; Live 0; Mismatches 32; Indels 0.
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APPLICANT: CROWE, JAMES SCOTT
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
STREET: 555 THIRTERNTH ST. N.W.
CITY: WASHINGTON
STREET: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: anti-Rh(D) antibody clone SH28
US-09-240-274-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
Sequence 207, Application US/09240274
Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08378939
Patent No. 5876961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 CAAGGIGGAAATCAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 CAAGGTGGAAATCAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-378-939-13
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Best Local 9
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377

APPLICATION NUMBER: US/08/378,939 FILLING DATE:

CURRENT APPLICATION DATA

REFERENCE/DOCKET NUMBER: 1808-118 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 783-6040

INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 321 base pairs TYPE: mucleic acid STRANDEDNESS: both

linear

MOLECULE TYPE: HYPOTHETICAL: N ANTI-SENSE: NO

TOPOLOGY:

CDS

NAME/KEY: LOCATION:

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181 AGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 201, Application US/09240274;
Patent No. 625455
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL;
TITLE OF INVENTION: SCATING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SCATING METHOD FOR PRODUCTION THEREOF
TITLE OF INVENTION: SCATING METHOD FOR PRODUCTION THEREOF
GURRENT APPLICATION NUMBER: US/09/240,274
GURRENT PILING DATE: 1999-01-29
SARLIER PILING DATE: 1998-04-10
EARLIER PILING DATE: 1998-04-10
SARLIER PILING DATE: 1998-04-10
SARLIER PILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
                                                                                                                                                                                                                                                                                                                              61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAATTTAAATTTGGTATCAAGAAAACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCACATTTT 180
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                                                                                                                                                                                                                                                                                            61 ATCACTTGCAGGGCAAGTCAGGACATTAGGTATTTTAAATTGGTATCAGCAGAAACCA 120
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                                                                                                                                                                                                             1 GACATCCAGATGACCCAGTCTCCATCCTCTGCATCTGTAGGAGACAGAGTCACC
                                                                                                                                                                          1 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC
                                                                                                                    ;
0
                                                  81.6%; Score 261.8; DB 2; Length 321; 88.5%; Pred. No. 2.1e-78; tive 0; Mismatches 37; Indels 0
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                                                                                                                 Matches 284; Conservative
                                                                                     Similarity
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US-08-378-939-13
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RESULT 13
US-09-240-274-215
i Sequence 215. Application US/09240274
i CENERAL INFORMATION: APPLICANT: Siegel, Donald L.
i TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
i TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
i TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
i TITLE APPLICATION NUMBER: US/09/240,274
CURRENT APPLICATION NUMBER: US/09/240,274
i EARLIER PILLING DATE: 1998-04-19
i EARLIER PILLING DATE: 1998-04-10
i EARLIER PILLING DATE: 1998-04-10
i EARLIER PILLING DATE: 1996-10-11
i NUMBER OF SEQ ID NOS: 224
i SEQ ID NO 215
i LENGTH: 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 CAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACGTGAAGGTGAAGA 242
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81.5%; Score 261.6; DB 3; Length 321;
Best Local Similarity 89.2%; Pred. No. 2.4e-78;
Matches 282; Conservative 0; Mismatches 34; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Query Match

81.5%; Score 261.6; DB 3; Length 321;
Best Local Similarity 89.2%; Pred. No. 2.4e-78;
Matches 282; Conservative 0; Mismatches 34; Indels 0
                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
PERATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOTHER INFORMATION: anti-Rh(D) antibody clone SH46 US-09-240-274-215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 CAAGGTGGAAATCAAA 321
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 201
LENGTH: 321
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ORGANISM: Homo sapiens
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RESULT 15 US-09-240-274-211

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| Sequence 211, Application US/09240274
| Sequence 211, Application US/09240274
| Patent No. 6255455
| SEMERAL INFORMATION:
| APPLICANT: Siegel, Donald L.
| TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
| TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
| FILE REFERENCE: 09596-4207
| CURRENT APPLICATION NUMBER: US/09/240,274
| CURRENT FILING DATE: 1999-01-19
| EARLIER APPLICATION NUMBER: 60/081,380
| EARLIER PILING DATE: 1999-01-0
| EARLIER PILING DATE: 1996-10-11
| NUMBER OF SEQ ID NOS: 224
| SOFTWARE: PatentIN Ver. 2.0
| SEQ ID NO 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 AGCTCCTAAGCTCCTGATCTATGTATCCAGTTTGCAAAGTGGGAGTCCCATCAAGGTT 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 ITTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGGAC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 TITIGCAACTIACTACTGTCAACAGAGTTACAGTACCCCTCCGGCTTTCGGCCCTGGGAC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 CCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCAC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
81.0%; Score 260; DB 3; Length 321;
Best Local Similarity 88.9%; Pred. No. 8.3e-78;
Matches 281; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGAN:SM: Homo sapiens FEATURE: OTHER INFORMATION: anti-Rh(D) antibody clone SH36 US-09-240-274-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 CAAGGTGGAAATCAAA 321
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Search completed: June 19, 2004, 05:42:26 Job time: 65 secs

App App Appli

Sequence

Sequence 201, App Sequence 215, App Sequence 217, App Sequence 21, App Sequence 211, App Sequence 121, App Sequence 129, App Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 26, Appl Sequence 27, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 36, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 213, Appl Sequence 36, Appl

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61 ATCACTTGCAGGCCAAGTCAGGACATTAGGTATTTAAATTGGTATCAGCAGAAACCA
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US-09-848-798-104
US-09-848-798-207
US-09-848-798-201
US-09-848-798-201
US-09-848-798-215
US-09-848-798-215
US-09-848-798-215
US-09-848-798-215
US-09-848-798-215
US-09-848-798-215
US-09-848-798-219
US-09-848-798-109
US-09-848-798-109
US-09-848-798-105
US-09-848-798-106
US-09-848-798-106
US-09-848-798-205
US-10-091-300-32
US-09-848-798-205
US-09-848-798-203
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Pred. No. 1.3e-80;
0; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-63-244-78

US-10-63-244-78

Sequence 78, Application US/10663244

Publication No. US20040110933A1

GENERAL INFORMATION:
APPLICANT: Rondon, Isaac J.
APPLICANT: Rondon, Isaac J.
APPLICANT: Rendon, Isaac J.
TITLE APPLICANT: Rendon, Isaac J.
TITLE REPRENCE: 10280-063001

CURRENT APPLICATION NUMBER: US/10/663,244

CURRENT FILING DATE: 2003-09-15

PRIOR PRILING DATE: 2002-09-13

PRIOR PRILING DATE: 2002-09-13

PRIOR PRILING DATE: 2003-05-09

NUMBER OF SEQ ID NOS: 165

SOFTWARE: ReasERD for Windows Version 4.0

SEGOTUMARE: 321
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ORGANISM: Artificial Sequence
         Query Match
Best Local Similarity
Matches 290; Conserv
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-848-798-102
US-09-848-798-218
US-09-848-798-221
US-10-172-317-3
US-10-320-094-3
US-10-320-094-3
US-09-848-798-105
US-09-848-798-105
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i Sequence 102, Application US/09848798
i Publication No. US2030040605A1
i GENERAL INFORMATION:
J APPLICANT: Siegel, Donald L.
J TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
ITITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
ILLE REFERENCE: 09596-4202
CURRENT FAPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR PILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 102
LENGTH: 321
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                                                 121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTCCAAAGTGGGGTCCCATCA 180
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US-09-848-798-102
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Matches 287; Conservative
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ORGANISM: Homo sapiens
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RESULT

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Sequence 218, Application US/09848798

Publication No. US20030040605A1

Publication No. US20030040605A1

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF TRIBNED DATE: US/09/848,798

CURRENT APPLICATION NUMBER: US/09/848,798

CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/240,274

PRIOR PRIDE DATE: EARLIER FILING DATE: 1999-01-29

PRIOR PREDICATION NUMBER: BARLIER PILING DATE: 1999-01-29

PRIOR PREDICATION NUMBER: BARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SEQ ID NO 218

LENGTH: 321
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| Publication No. US20030040605A1
| GENERAL INFORMATION:
| APPLICANT: SLEGEI, Donald L.
| TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL:
| TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
| FILE REFERENCE: 09596-4202
| CURRENT APPLICATION NUMBER: US/09/848,798
| CURRENT PILING DATE: EARLIER RABILER APPLICATION NUMBER: 09/240,274
| PRIOR APPLICATION NUMBER: EARLIER PLING DATE: 1999-01-29
| PRIOR APPLICATION NUMBER: EARLIER PLING DATE: 1996-10-11
| NUMBER OF SEQ ID NOS: 224
| SEQ ID NO 221
| LENGTH: 321
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US-09-848-798-218
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90.8%; Pred. No. 5.1e-80;
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Best Local Similarity 90.8
Matches 287; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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  123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182
                                                                                                                                   TITIGCGACTIATIACTGICTACAGGITTATAGIACCCCTCGGACGITCGGCCAAGGGAC 305
                                                                                                                                                                    243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGAC 302
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                                                                                  183 CAGIGGCAGIGGAICIGGGACAGAITTCACICICACCAICAGCAGICIGCAACCIGAAGA
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APPLICANT: van Dijk, Marcus A.
APPLICANT: van Dijk, Marcus A.
APPLICANT: HILK, Edward
APPLICANT: Gerritean, Arnout F.
TITLE OF INVENTION: HUMAN MONOCIONAL ANTIBODIES TO
TITLE OF INVENTION: BPIDERMAL GROWTH FACTOR RECEPTOR
FILE REFERENCE: GMT-020
CURRENT APPLICATION NUMBER: US/10/172,317
CURRENT FILING DATE: 2002-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASLEEQ for Windows Version 4.0
SEQ ID NOS: 4
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Pred. No. 1.5e-79;
0; Mismatches 33; Indels
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Best Local Similarity 89.7%;
Matches 288; Conservative
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CRGANISM: Homo sapiens
US-10-172-317-3
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TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: BACELIER FILING DATE: 1996-10-11
SOFTWARE: BACELIER FILING DATE: 1996-10-11
SOFTWARE: BACELIER FILING DATE: 1296-10-11
LINGBER OF SEQ ID NOS: 224
LENGTH. 321
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                                                                                                                84.0%; Score 269.6; DB 10; Length 321; 90.8%; Pred. No. 5.1e-80; ive 0; Mismatches 29; Indels 0;
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) ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-221
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; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-222
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                                                                                                                   Query Match
Best Local Similarity 90.8
Matches 287; Conservative
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ORGANISM: Homo sapiens
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US-09-848-798-222
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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 105
US-09-848-798-105
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; Sequence 105, Application US/09848798
; Publication No. US20030040605A1
; Publication No. US20030040605A1
; GENERAL INFORMATION: N. US20030040605A1
; TITLE OF INVENTION: Rh.(D)-BINNING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: Rh.(D)-BINNING PROPERIOR THEREOF
; TITLE OF INVENTION: N. WHORE: 105/09/848,798
; CURRENT APPLICATION NUMBER: 2001-05-04
; FILE REFERENCE: DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: BARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: BARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PALENTING DATE: 1996-10-11
; SEQ ID NO 105
; SEQ ID NO 105
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APPLICANT: van de Winkel, Jan G.J.
APPLICANT: van Dijk, Marcus A.
APPLICANT: van Dijk, Marcus A.
APPLICANT: Gerriten, Arnout P.
APPLICANT: Gerriten, Arnout P.
APPLICANT: Gerriten, Arnout P.
TILLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
TITLE OF INVENTION: ENDIBREMAL GROWTH FACTOR RECEPTOR
TITLE OF INVENTION UNMERR: US/10/320,094
CURRENT APPLICATION NUMBER: US 6/298172
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 12
SAGTHARS: PSECSO for Windows Version 4.0
SEQ ID NO 3
LENGTH: 321
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89.7%; Pred. No. 1.5e-79;
ive 0; Mismatches 33;
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Best Local Similarity 89.7
Matches 288; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-320-094-3
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                                                                                                                    3 caacricaccagricaccarcciccrererecarcrasaaaaaaaaaacaaaacacarcac
                                         Gaps
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; Publication No. US20030167502A1
; Publication No. US20030167502A1
; GARREAL INPORMATION:
   APPLICANT: Dec. Yashwant M.; APPLICANT: Reler, Tibor
   TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
   TITLE OF INVENTION: GELS;
   FILE REFERENCE: MXI-65
; FURRENT FILING DATE: 2001-05-08
; PRIOR FILING DATE: 2000-05-08
; PRIOR PLING DATE: 2000-05-08
; PRIOR FILING DATE: 2000-05-07
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 321
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Pred. No. 5.2e-79;
0; Mismatches 34;
Score 268; DB 10;
Pred. No. 1.8e-79;
0; Mismatches 30;
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Best Local Similarity 89.4%;
Matches 287; Conservative
    Query Match
Best Local Similarity 90.5%;
Matches 286; Conservative
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FRATURE:
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; LOCATION: (1)
US-09-851-614-1
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                                                                                                  APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: RA(D) BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REPERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT PILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATEUR PATEUR PATEUR
EARLIER FILING DATE: EARLIER FILING DATE: 1966-10-11
LENGTH: 321
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US-09-848-798-216
US-09-848-798-216
; Sequence 216, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RA(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATE
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 05596-42D;
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: RARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: BARLIER FILING DATE: 1999-01-29
; PRIOR FILING DATE: BARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PALENTIN Ver. 2.0
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Pred. No. 6.1e-79;
0; Mismatches 31;
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; CTHER INFORMATION: anti-Rh(D) chain I07
US-09-848-798-107
                                                Sequence 107, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
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Best Local Similarity 90.2%;
Matches 285; Conservative (
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                                  JS-09-848-798-107
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GAGAAAGCCCCTAAGTCCCTGATCTATGCTGCATCCGGTTTGCAAAGTGGGGGTCCCATCA
                                                                         GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA
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Pred. No. 5.2e-79;
0; Mismatches 34;
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Best Local Similarity 89.4%;
Matches 287; Conservative (
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; LOCATION: (1)...(321)
US-10-035-637-1
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Sequence 98, Application US/09848798
Sequence 98, Application US/09848798
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITE OF INVENTION: RN 10)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42UZ
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR PAPLICATION NUMBER: GARLIER APPLICATION NUMBER: 09/240,274
PRIOR PLING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR PLING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 98
LENGTH: 321
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Length 321;
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Best Local Similarity 89.9%; Pred. No. 2.1e-78;
Matches 284; Conservative 0; Mismatches 32;
   82.6%; Score 265; DB 15;
ilarity 89.1%; Pred. No. 1.8e-78;
Conservative 0; Mismatches 35;
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OTHER INFORMATION: anti-Rh(D) chain F01
US-09-848-798-98
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ORGANISM: Homo sapiens
         Query Match
Best Local Similarity
Matches 286; Conserv
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                                                                                                                                                                                                                               Length 321;
                                                                                                                                                                                                                                                                                          31; Indels
                                                                                                                                                                                                                               83.0%; Score 266.4; DB 10;
llarity 90.2%; Pred. No. 6.1e-79;
Conservative 0; Mismatches 31;
                                                                                                                                   OTHER INFORMATION: anti-Rh(D) antibody clone SH47 US-09-848-798-216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRUERCE J. Application US/10060585
Publication No. US20030083290A1
GRNERAL INFORMATION
JEDPLICANT: Kingsman, Alan J.
APPLICANT: Carroll, Miles W.
APPLICANT: Carroll, Miles W.
APPLICANT: Bland, Fiona M.
APPLICANT: Britan, Susan M.
APPLICANT: Kingsman, Susan M.
APPLICANT: Kingsman, Susan M.
APPLICANT: Kingsman, Susan M.
APPLICANT: Kingsman, Susan M.
APPLICANT: Wyers, Kevin A.
TILLE OP INVENTION: UNCORP.
CURRENT APPLICATION NUMBER: US/10/060,585
CURRENT APPLICATION NUMBER: US/060,585
CURRENT PLING DATE: 1998-06-04
FRICR FILING DATE: 1998-06-04
FRICR FILING DATE: 1998-06-04
FRICR FILING DATE: 1997-07-04
FRICR FILING DATE: 1997-07-04
FRICR FILING DATE: 1997-06-04
FRICR FILING DATE: 1997-07-04
FRICR APPLICATION NUMBER: GB 9713150.2
FRICR FILING DATE: 1997-01-13
FRICR FILING DATE: 2000-11-13
FRICR FILING DATE: 1999-11-18
FRICR FILING DATE: 1999-11-18
FRICR FILING DATE: 1999-11-18
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), OTHER INFORMATION: Anti-TWF alpha
US-10-060-585-9
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                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 285; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 9
LENGTH: 321
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US-10-060-585-9
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Gaps

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Sequence 104, Application US/09848798

Sequence 104, Application US/09848798

Publication No. US20030040605A1

GENERAL INFORMATION:

APPLICANT: Siegel 1.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TILE OF INVENTION NUMBER: US/09/848,798

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/240,274

PRIOR PILING DATE: BARLIER FILING DATE: 1999-01-29

PRIOR FILING DATE: RARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NCS: 224

SEQ ID NO 104

LENGTH 321

LENGTH 321
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246 TITTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGGAC 305
243 TTCTGCCAACTTATTACTGTCTACAGCATAATAGTTTCCCGTGGACGTTCGGCCAAGGGAC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TIGCAGGGCAAGTCAGGACATTAGGTATTAAATTGGTATCAGCAGAAACCAGGAAA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 TITTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGGAC 305
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CTHER INFORMATION: anti-Rh(D) chain 104

US-09-848-798-104
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                                                                                                                                                         303 CAAGGTGGAAATCAAA 318
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                            RESULT 15
US-09-848-798-104
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Search completed: June 19, 2004, 06:26:45 Job time : 286 secs

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June 19, 2004, 04:30:43; Search time 1734 Seconds (without alignments) 5528.120 Million cell updates/sec
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1 gacatccagatgacccagtc......ggaccaaggtggaaatcaaa 321
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 321
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES			ID		AW404590	BF869849	AW406247	AW406545	
			DB		2	10	10	10	
			Match Length DB	1 1 1 1 1 1 1	269	284	270	315	
	οķο	Query	Match		69.7	67.5	66.5	65.2	
			Score		223.6	216.8	213.4	209.4	
		tesalt	Š.	1 1 1 1 1 1	П	0	m	41	

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AW406058	AA300031	AA300788	BF095147	AW407313	BF869187	AA377295	AW404303	BM856175	CD686963	AW407923	AA300491	BE720151	AW404355	BE163116	BF870341	BM825516	AA295508	BF869666	CD709351	AW860832	AA301343	BF870338	AW404283	AW951839	CD690814	BM769908	AA327542	CD708479	AW405131	BF868804	AW366663	AA295841	AW404261	AW800017	AA366827	CD706092	CD693795	BM823161	T27581	AW407044
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	mRNA 1	UI-HF-BLO-acb-d-03-0-UI.rl NIH_MGC_37 Homo sapiens						Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	Primates; Catarrhini; Hominidae; Homo.			National Institutes of Health, Mammalian Gene Collection (MGC)				Eco RI site shown at the beginning of the sequence.	it, M.D.,	cDNA Library Preparation: M.B. Soares Lab	res Lab	•	Clone distribution: MGC clone distribution information can	found through the I.M.A.G.E. Consortium/LLNL at:	tml	
	269 bp	NIH MGC	dence.					ata; Crani	ces; Catan		gov/.	alth, Mamm		3, Ph.D.	yor	seginning	M. Stauc	: M.B. So	cDNA Library Arrayed by: M.B. Soares Lab	Joares Lak	clone dist	E. Consoi	je/image.k	
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		acb-d-0		69:ID 1		ans (hum	sus	Metazo	Butheri	1 to 26	:tp://md	Institut	6661) pa	Robert Si	pps-rem	e shown	cocuremen	ary Pre	ary Arr	ncing b	tribution	ough the	nl.gov/l	C: M13 F
	AW404590	UI-HF-BLO	IMMOBISCOSOGO S., MANA Bequence: AW404590	AW404590.1 GI:6923647	EST.	Homo sapiens (human)	Homo sapiens	Bukaryota	Mammalia; Butheria;	1 (bases 1 to 269)	NIH-MGC http://mgc.nci.nih.gov/.	National :	Unpublished (1999)	Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov	Eco RI sit	Tissue P	CDNA Lib	CDNA Lib	DNA Seque	Clone die	found thro	www-bio.lln[.gov/bbrp/image/image.html	Seg primer: M13 Forward.
RESULT 1 AW404590	FOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT										
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AW406247
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DEFINITION
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1 (Dases 1 to 204)
Diasses 1, to 204)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 223.6; DB 10; Length 269;
Pred. No. 2.1e-62;
0; Mismatches 24; Indels 0;
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                'organism="Homo sapiens"
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Socation/Qualifiers
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Best Local Similarity 90.8%;
Matches 238; Conservative C
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Pax: +55-11-2707001
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Homosapiens
Homanalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (hases 1 to 270)
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. B. Soares Lab
DNA Sequencing by: M. B. Soares Lab
DNA Sequencing by: M. B. Soares Lab
DNA Sequencing by: M. B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILJ&t2=ILJ-ET0114-251000-317-G07k5=2000-0.26t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 185.

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UI-HF-BLO-acp-e-11-0-UI.rl NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3059828 5', mRNA sequence.
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Gabs

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Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

Homenalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 254)

NIH-MCD http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (M3C)

Li Unpublished (1999)

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Email: capaba-remail.nih.gov

Exo RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G. E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: MI Forward.

Seq primer: MI Forward.
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(1.5-2.Skb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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MGC_37 Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                 65.2%; Score 209.4; DB 10; Length 315; 89.6%; Pred. No. 1.1e-57; ive 0; Mismatches 26; Indels 0;
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UI-HF-BLO-ach-e-01-0-UI.rl NIH_N
IMAGE:3059040 5', mRNA sequence.
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Matches 225; Conservative
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
El (bases I to 115)
I (bases I to 115)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Econtact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Contact: Preparation: M.B. Soares Lab
CONA Library Preparation: M.B. Soares Lab
CONA Library Preparation: M.B. Soares Lab
CONA Library Arrayed by: M.B. Soares Lab
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at:
www-bio.llhl.gov/bbrp/image.html
Seq primer: Mil Forward.
Seq primer: Mil Forward.
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Constructed from size fractionated cytoplasmIc mRNA
Constructed from size fractionalty cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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UI-HF-BL0-acu-e-04-0-UI.rl NIH MGC_37 Homo sapiens cDNA clone
INAGE:3060199 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 GCCCCTAAGCTCCTGATCTACGATCCCAATTTGGAAACAGGGTCCCATCAAGGTTC 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 CAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.5%; Score 213.4; DB 10; Length 270; 88.2%; Pred. No. 4.7e-59; ive 0; Mismatches 31; Indels 0;
www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward.
                                                                                                 /organism="Homo sapiens"
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/clone="IMAGE:3059828"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 ATTGCAACATATTACTGTCAACA 270
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Best Local Similarity 88.2
Matches 232; Conservative
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/clone="TMAGE:3059040"
/tissue_type="lymph"
/cell type="germinal center B cells"
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Constructed from size fractionaled cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA300891 303 bp mRNA linear EST 18-APR-1997 EST4031 Testis tumor Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region, mRNA sequence. AA300891
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                                                                                                                                                                                                                                                                                 61 ATCACTIGCAGGCAAGTCAGGACATTAGGTATTATATAAATTGGTATCAGCAGAAACCA 120
                                                                                                                                                                                                                                                                                                                                   121 GGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTCCCATCA 180
143 GGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCGATTTGCAAGTGGAGGTCCCATCA 202
                                                                                                                                                                                                                                                                                                  83 ATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTAGGCTGGTATCAGCAGAAACGA 142
                                                                                                                                                                                                                                1 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTCTGTAGGGGACAGAGTCACC 60
                                                                                                                                                                                                                                                 23 GACATCCAGATGACCCAGTCTCCATCCTCCCTGCATCTGTAGGAGACAGAGTCACC 82
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                                                                                                                                                                                 Length 254;
                                                                                                                                                                              63.8%; Score 204.8; DB 10; Length llarity 92.7%; Pred. No. 3.1e-56; Conservative 0; Mismatches 17; Indels
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Contact: Kerlavage, AR
Bioinformatics
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Homo sapiens
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Best Local Similarity
Matches 215; Conserva
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Homo sapieus brimata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 303)

2 Adams, M. D., Kerlavage, A. R., Fleischmann, R. D., Fuldner, R. A.,
Bult, C. J., Lee, N. H., Kirkness, E. F., Weinstock, K. G., Gocayne, J. D.,
White, O., Sutton, G., Blake, J. A., Brandon, R. C., Man. Wai, C.,
Fitzgerald, L. M., Fitzhud, W. M., Pritchman, J. L., Geoglagen, N. S.,
Fitzgerald, L. M., Fitzhud, W. M., Pritchman, J. L., Geoglagen, N. S.,
Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, P. S., Gr.
Kelley, J. M., Kelley, J. C., Liu, L. I., Marmaros, S. M., Merrick, J. M.,
Noreno-Palanques, R. P., McDonald, L. A., Nanyven, D. T., Pelligrino, S. M.,
Phillips, C. A., Ryder, S. B., Scott, J. L., Saudek, D. M., Shirley, R.,
Small, K. V., Spriggs, T. A., Utterback, T. R., Weidman, J. F., Li, Y.,
Bednarik, D. P., Feng, D. F., Perris, A., Fischer, C., Hastings, G. A.,
Kozak, D. L., Kunsch, C., Hungjun, J., Li, Hudson, P., Kim, A.K.,
Raymond, L., Wei, Y. P., Wing, J., Xu, C., Yu, G. L., Ruben, S.M.,
Braser, C. M. and Venter, J. C.
Rasen, C. M., Haseltine, W. A., Fields, C.,
Fraser, C. M. and Venter, J. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA300788 303 bp mRNA linear EST 18-APR-1997 EST13648 Testis tumor Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region, mRNA sequence.
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The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA 19712 Medical Center Drive, Rockville, MD 20850 USA 19713 Medical Center Drive, Rockville, MD 20850 USA East: 3018699423 Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlated to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MJ3 Reverse.
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| forgatism="Homo sapiens" |
| forgatism="Homo sapiens" |
| forgatism="Homo sapiens" |
| fub_xref="ATCC (inhost):191887" |
| fub_xref="AXCM:9606" |
| fub_xref="adult" |
| fub_melle" |
| fub_mell
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Best Local Similarity 91.1%; Pred. No. 7.3e-56;
Matches 214; Conservative 0; Mismatches 21;
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Tel: +55-11-2704922
Pax: +55-11-2700001
Pax: +55-11-2700001
This sequence was derived from the PAPESP/LICR Human Cancer Genome Strips sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM3-UT0058-060 900-004-e03&t3=2000-09-06&t4=1)
Seq primer: put 18 forward
High quality sequence start: 15
High quality sequence stop: 276.
High quality sequence stop: 276.

1. .276
/organism="Homo sapiens"
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1 (Dases 1 to 280)
WIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAGICTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 62.3%; Score 200; DB 10; Length 276; al Similarity 91.4%; Pred. No. 1.2e-54; 234; Conservative 0; Mismatches 20; Indels 2
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1 (Bases I to 276)

1 (Baroia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Garcia Correa,R., Verjovski-Almeida,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsıkuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., Geoliveira,P.S., Bucher,P., Jongeneel,C.V., Go'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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mRNA sequence.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 GAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCAA 181
                                                                                                                                             Other ESTS: THC167177
Contact: Kerlavege, AR
Boinformatios
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Fil: 3018699623
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/clone lib="Testis tumor"
/note="Organ: testis; Vector: pBluescript SK-; Site_1:
Book!, Site_2: Xho!"
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 203.6; DB 9; Lems...
Pred. No. 8.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
|mol_type="mkma"
|db xref="ATCC (inhost):192224"
|db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.4%; Score 203.6;
ilarity 91.5%; Pred. No. 8.5e
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
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VERSION
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1. 304
| Organism="Homo sapiens"
| / organism="Homo sapiens"
| / db _xref="taxon:9606" |
| / db _xref="taxon:9606" |
| / dev etage="Adult" |
| / dlone lib="270115" |
| / lone="organ: lung tumor; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from CRESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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BST89837 Small intestine II Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region, mRNA sequence.
                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPBSP/LICR Human Cancer Genome
This sequence was derived from the Fallowing UR.

Project. This entry can be seen in the following UR.

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL3&t2=IL3-ET0115-
181000-294-F05&t3=2000-10-18&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TIGCAGGCAAGICAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAA 125
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                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ccaeareacccaercrecerecerererererererandeacaeacaercaecareac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 304;
          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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llarity 82.5%; Pred. No. 1.1e-53;
Conservative 0; Mismatches 48; Indels
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High quality sequence stop: 303.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"

/mol_type="mkNx"

/db_xref="taxon:9606"

/db_xref="taxon:9606"

/clone="taxon:9606"

/clone="type="taxon:9606"

/cell_line="McG68"

/cell_line="McG68"

/lab_host="bH10B (LTI)"

/clone=lib="WHH MGC 37"

/note="Vector: pT773-Pac; Site_1: Not1; Site_2: Eco RI;

/note: pT773-Pac; Site_1: PT773-Pac;

/note: pT773-Pac; Site_1: PT773-Pac;

/note: pT773-Pac; Site_1: PT773-Pac;

/note: pT773-Pac;

/note: pT773-Pac;

/note: pT773-
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(Dases 1 to 304)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., Gordin,S., Ostet,F., Nagai,M.A., Bordin,S., Coste,F., Erustein,A., Garvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., Geoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAAAGCCCCTAAGCTCCTGATCTATAAGGCATCTAGTTTAGAAAGTAAAGTTCCATCA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 AGGTTCAGCGGCAGTGGATCTGGGAATTCACTCTCACCATCAGCAGCCTGCAGCAGCT 262
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                            Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information (found through the I.M.A.G.B. Consortium/LLML at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward
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Pred. No. 3.1e-54;
0; Mismatches 37; Indels
Contact: Robert Strausberg, Ph.D.
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Cone lib=*NIH MGC 37"

/note="Vector: PTTT-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionalted cytoplasmic mRNA

Constructed from size fractionaled cytoplasmic mRNA

(15-2.8hb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (2012) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (2014) (
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/cell_type="germinal center B cells"
/cell_line="MGC85"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3058609"
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Bult, C.J., Lee, N.H., Kirkmess, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, B. Hinhle, P. S.T., Kelley, J. M., Kelley, J. C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.J., Saudek, D.M., Shiley, R., Small, K.V., Spriggs, T.A., Ulterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, S.J., Dimke, D., Fangy, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymord, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruber, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million mucleotides of CDNA sequence
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
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/note="Organ: small intestine; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
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89.0%; Pred. No. 3.7e-53;
ive 0; Mismatches 26; Indels 0
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9712 Medical Center Drive, Rockville, MD 20850 USA
7E1: 3018699056
Fax: 3018699423
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/mol_type="mRNA"
/db_xref="ALC" (inhost):181687"
/db_xref="taxon:9606"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other ESTs: EST89836 THC167177
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104

Gaps

164

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Homo sapiens (human)
Homo sapiens
                                                             Unpublished (2003)
Contact: YiXin Zeng
Cancer Center
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//note="Organ: Stoned: Vector: pT218RP1; Site 1: ECORI;
Site 2: Not1; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact manA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about Gont. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli ToplOf' by electroporation method.
The cDNA libraries constructed by this method are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCAACTGTAGGAGACAGAGTCACC 149
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 276)
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Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean BST Project 2001
Unpublished (2002)
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EST3484 human nasopharynx Homo sapiens cDNA, mRNA sequence
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                                                                                                         Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="s14K402-53-D11"
/cell_line="K402"
/lab_nost="Topl0F"
                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                              Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 53 row: D column: 11
                                                                                                                                                                                                                                                           High quality sequence stop: 321.
Location/Qualifiers
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                                                                                           Contact: Kim YS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Rummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Lases 1 to 252)

2 In (Lases 1 to 252)

3 In Hack tip://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

4 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LINL at:

Wow-bio.llnl.gov/bbrp/image/image/image.html

Seq primer: Mil Forward.
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UI-HE-BLO-add-c-07-0-UI.r2 NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3061236 5', mRNA sequence.
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Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GACATCCAGATGACCCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC
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                                                                                                                                                                                Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-245456
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
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Best Local Similarity 89.9%; Pred. No. 2.1e-51;
Matches 204; Conservative 0; Mismatches 23.
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(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatina
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Best Local Similarity 92.2%; Pred. No. 2.7e-51;
Matches 200; Conservative 0; Mismatches 17; Indels 0;
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Search completed: June 19, 2004, 05:41:24 Job time : 1748 secs

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June 19, 2004, 07:32:38; Search time 1845 Seconds (without alignments) 8316.224 Million cell updates/sec
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1 gaggtgcagctggtggagtc......tcctggtcaccgtctcctca 354
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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No.
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348 bp mRNA linear PRI 11-OCT-2003 Homo sapiens clone 56-58a Ig heavy chain variable region, VH3 family mRNA, partial cds.

AF471251.1 GI:33319045 Homo sapiens (human)

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

is the number of results predicted by chance to have a

N N

Pred.

DEFINITION

RESULT 1 AF471251

ALIGNMENTS

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 348)
Scamura, R.W., Nelson, D.B., Miller, D.J., Lorenz, E. and Janoff, E.N.
Impact of HIV-1 on Somatic Hypermutation in Mucosal B Cells

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Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
Unpublished
2 (bases I to 348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U00491 348 bp mRNA linear PRI 08-MAY-1994
Human immunoglobulin heavy chain variable region (clone Amulc3-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TCCTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAAFAACTACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTAGTACTACATA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CAGGCTCCAGGGCCAGGGGCTGGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
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                                                                                                                                                                                   Extrosawa.Y.
Direct Submission

Loudited (25-dun-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyoake 470-1192, Japan
(E-mail: kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.

I . 348
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peripheral blood and bone marrow"
fammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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295 GGTTGGGGAACCCTTGACTACTGGGGGCCAGGGAACCCTGGTCACGGTCACGGTCTC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.6%; Score 246.4; DB 9; Length 348; Best Local Similarity 83.7%; Pred. No. 2.1e-55; Matches 293; Conservative 0; Mismatches 51; Indels 6;
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                                                                                                                                                                                       //OSGILOTYPE="MENA"
//ASGILOTYPE="MENA"
//ASGILOTYPE="MENA"
//ASGILOTYPE="MENA"
//ASGILOTYPE="IGA plasma cell"
//Lissue_type="IgA plasma cell"
//Lissue_type="HIV positive"
//Lissue_type="HIV positive"
//Lissue_type="Ighavy chain variable region, VH3 family"
//Protein_id="AAQ05426.1"
//Protein_id="AAQ05426.1"
//LISSUEGETIFYADSVKGRFTISRDNAKNSLYZCAASGFTFSHYYYSWIRQAPGKG
LEWILYISSSGGTIVADSVKGRFTISRDNAKNSLYZCARASFY
PDYWGGGTLVTVSS"
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AB063673. GI:21668547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 AGGCTCCAGGGAAGGGGCTGGAGTGGCTTTATATACATTAGTAGTAGTAGTAGTAGTACTATATT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
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                                       and Janoff, E.N.
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                    Scamura, R. W., Nelson, D.B., Miller, D.J., Lorenz, B. and Janoff, Scamura, R. W., Nelson, D.B., Miller, D.J., Lorenz, B. and Janoff, Direct Submission
Submitted (22-JAN-2002) Division of Infectious Diseases-111F, Nucosal and Vaccine Research Center, Veterans Affairs Medical Center, Location/Qualifiers
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296 CAAGCCCCTACTTGACTACTGGGGCCAGGGAACCCTGGTCACGTCTCCTCA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 348;
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Pred. No. 3.4e-56;
0; Mismatches 51; Indels
                                                                                                                                                        1. .348
/organism="Homo sapiens"
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/note="V3-11"
295. .315
/note="CDR3 region"
303. .348
/note="J4b"
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Best Local Similarity 83.9%;
Matches 296; Conservative
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                                                                                                                                      Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 348)

Glas, A.M., van Montfort, E.H.N., Storek, J., Green, E.N.,

Drissen, R.P., Bechtold, V.J., Reilly, J.2., Dawson, M.A. and

Milner, E.C.B.
Homo sapiens clone 1-3 immunoglobulin heavy chain variable region
MRNA, partial cds.
AF221396
                                                                                                                                                                                                                                                                                                                                                                  B cell-autonomous somatic mutation deficit following bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 Tactacecacactecereaaeseceerrecaceareceareceaeaaeaarecace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
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/note="V3-23"
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Matches 292;
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/product="immunoglobulin heavy chain variable region"
/protein id="AAA17905.1"
/db_xref="61:392578"
/translation="BYQLLESGGGLVQPGGSIRLSCAASRFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLXLQMNSLRAEDTAVYYCAMVGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRI 13-JUN-2000
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1 (bases 1 to 348)

Huang, C. and Stollar, B.D.

A majority of 1g H chain cDNA of normal human adult blood lymphocytes resembles cDNA for fetal 1g and natural autoantibodies J. Immunol. 151 (10), 5290-5300 (1993)
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Stollar,B.D.
Direct Submission
Submitted (10-AUG-1993) Stollar B.D., Tufts University,
Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA
Location/Qualifiers
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Pred. No. 3.5e-55;
0; Mismatches 54; Indels 6;
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/tissue type="peripheral blood"
/clone_lib="Amu2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 348
/organism=Rhomo sapiens"
/organism=Rhomo sapiens"
/nol_type="mRNA"
/db xref="texon:9606"
/clone="Amulc3-3"
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Best Local Similarity 83.1%;
Matches 294; Conservative
                                                                                                                                Homo sapiens (human)
Homo sapiens
                                                U00491
U00491.1 GI:392577
                      mRNA, partial cds.
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348 bp mRNA linear PRI 27-MAR-2002
Homo sapiens mRNA for immunoglobulin heavy chain variable region
AB021526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein id="BAA36318.1"
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PDYWGGGTLYTVS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAGGCCAACAACAACAACAACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 CTGTATCTGCAAATGAACAGCCTGAGAGCGGAGGACACGCGCGTATATTACTGTGCGAAA 294
                                                                                                                                                   Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIGITICITICAAAIGAACAGCCIGAGAGCIGAGGACACGGCIGICIATIACIGIGGGAGC 300
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                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (18-DEC-1998) Masayuki Hakoda, Tokyo Women's Medical
Submitted (18-DEC-1998) Masayuki Hakoda, Tokyo Women's Medical
University, Institute of Rheumatology, 10-22 Kawada-cho
Shinjuku-ku, Tokyo 162-0054, Japan
(B-mail:ratokyosmomo.so-net.or.jp, Tel:81-3-5269-1725,
Fax:81-3-5269-1726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGGTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="B cell"
| ... ->48
|/codon start=1
|/product="immunoglobulin heavy chain variable region
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295 GGGGAACTCGCTTTTGATTACTGGGCCAGGGAACCCTGGTCACGTCTCCTCA 348
                                                                                                                                                                                                                     Hakoda, M., Taniguchi, A., Kotake, S., Higami, K., Ichikawa, N., Silverman, G.J. and Kamatani, N. Pathogenic implication of a prototype B cell superantigen, espaiyalocacal protein A, in rheumatoid arthritis
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/mol_type="mRNA"
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                                                                                              AB021526.1 GI:4107065
                                                                                                                                Homo sapiens (human)
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2 (bases 1 to 348)
Hakođa,M.
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Best Local Similarity
Matches 291; Conserv
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HSICHADI3 348 bp mRNA linear PRI 17-JUL-1996
H.sapiens mRNA for variable immunoglobulin heavy chain, clone 3.
X98751
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/db_xref="G1:1430805"
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/db_xref="EBMTREMEL:CAA67302"
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LEWVAAISGSGGSTYTADSVKGRFTISRDNSKNTLYLQANSLRAEDTAVYYCAKDKGS
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                                                                                                                                                                                                                                                                                                                        Dorsam, H.
Direct Submission
Submitted (24-UTN-1996) H. Dorsam, German Cancer Research Center,
Submitted (24-UTN-1996) H. Dorsam, German Cancer Research Center,
Diagnostics and Experimental Therapy Program, Recombinant Antibody
Group, INP 280, 69120 Heidelberg, FRG
Location/Qualifiers
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                                                             X98751.1 GI:1410804
heavy chain; immunoglobulin; variable region.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1. .>348
/codon_start=1
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chain"
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/product="variable immunoglobulin anti-Digoxigenin heavy
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                                                                                                                                                                                                              Dorsam,H., Kipriyanov,S., Welschof,M. and Little,M.
Isolation of an anti-Digoxigenin antibody out of an human IGM-Antibody library and expression in E.coli
Unpublished
2 (bases 1 to 348)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 348;
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316. .348
/note="PR4 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91. .105
/note="CDR1 domain"
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/note="CDR2 domain"
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/note="FR2 domain"
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/note="FR1 domain"
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/note="FR3 domain"
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AB066982 342 bp mRNA linear PRI 02-JUL-2002
Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
partial cds, clone:aims0023h.
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                                                                                                                                                                                                                                                     TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAGGACGACAACACA 240
                                                                                                                                                                    Akahori,Y., Iba,Y., Morino,K.; Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J., Mulra,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission

Submitted (25-JJJ-2001) Yoshikazu Kurosawa, Institute for Submitted (25-JJJ-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Immunology; Kutsukake-cho, Toyoake, Aichi 470-1192, Japan (E-mail: kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)

Please visit our web site
URL:http://www.tujita-hu.ac.jp/immunity/.
Location/Qualifiers

1. 342
/organism=Homo sapiens"
/mol type="mixNa" / db xref="taxon:9606"
/clone="aims0023h"
/clone="aims0023h"
/clone="aims0023h"
/clone="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
                                TCCTGCGCAGCCTCCGGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
                                                                       61 ICCTGTGCAGCCTCTG-----GAITCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TTGACTACAGGGTCTGACTCCTGGGGCAGTCCTGGTCACCGTCTCCTCA 354
295 GATCGGTATAGCAGCTCGTCCTGGGGCAACCCTGGTCACCGTCTCCTCA 348
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Unpublished
2 (bases 1 to 342)
Kurosawa,Y.
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Homo sapiens
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 348)

Glas,A.M.; Nottenburg,C. and Milner,E.C.
Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient

L. Clin. Exp. Immunol. 107 (2), 372-380 (1997)

10 97182739

10 9030878

2 (bases 1 to 348)

Glas,A.M.; Nottenburg,C. and Milner,E.C.B.
Direct Submission

Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSUB0150 348 bp DNA linear PRI 19-FEB-1997
Human immunoglobulin heavy chain variable region (V3-23) gene,
partial cds.
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/protein_id="AAC51065.1"
/db_xref="GI:1791143"
/translation="EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGXG
LEWYSAGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRYS
SSSWGGGTLVTVSS"
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                                                                                         TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 240
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CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTAGCACA 174
                                                                                                                       175 TACTACGCAGACTCCCGTGAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACAGG 234
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/ Organism="Homo sapiens"
/ mol_type="genomic DNA"
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/ colone="00194"
/ tissue type="peripheral blood"
/ tissue type="peripheral blood"
/ note="0019+ peripheral blood B cells obtained from a healthy subject; clone 75 in reference 1"
1. .348
/ gene="Way-23"
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/gene="V3-23"
/note="Ig VH3 heavy chain"
/codon_start=1
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Matches 290; Conserv
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HSU80154 345 bp DNA linear PRI 19-FEB-1997 Human immunoglobulin heavy chain variable region (V3-23) gene, partial cds.
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Glas,A.M., Nottenburg,C. and Milner,E.C.B.
Direct Submission
Submitted (22-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                62 CCTGTGCAGCCTCTG-----GATTCACCTTCAGTGACTACTACATGAGCTGGATCCGCC 115
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I chases 1 to 345
Glas, A.M., Nottenburg, C. and Milner, B.C.
Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient Clin. Exp. Immunol. 107 (2), 372-380 (1997)
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/ Organism="Homo sapiens"
/ wol_type="genomic DNA"
/ db_xref="taxon:9606"
/ chromosome="14"
/ clone="00301"
/ cell_type="CD19+ B cells"
/ tissue type="peripheral blood"
/ note="CD19+ peripheral blood B cells obtained from a healthy subject; clone 79 in reference 1"
1. .345
/ gene="W3-23"
                                                                                                                                                                                                                             2 AGGIGCAGCTGGTGGAGTCTGGGGGAGCTTGGTCAAGCCTGGAGGGTCCCTGAGACFCT
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294 ----TGGTAACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 342
                                                                                                                          Length 342;
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                                                                                                                        Score 238.6; DB 9;
Pred. No. 2.7e-53;
0; Mismatches 44;
    291. .298
/note="CDR3"
299. .342
/note="Jh element"
                                                                                                                          Query Match 67.4%;
Best Local Similarity 84.1%;
Matches 297; Conservative
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080154.1 GI:1791150
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Submitted (31-OCT-1991) F.M. Raaphorst, Division of Immunology,
Dept. of Immunohematology and Bloodbank, Academic Hospital Leiden,
Building 1, E3-Q. P.O.Box 9600, 2300 Leiden, THE NETHERLANDS
For related sequences see X62954-X62972, X53612-3, M37277,
Schroeder H.W. Dr. et al., Proc.Natl.Acad.Sci.USA, 87:6149(1990) &
Ichihara y. et al., Eur. J. Immunol. 18:649(1988).
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                                                                                                                                                                                                                                                                           175 TACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGGGACAAGGACAAGAACTCA 234
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Restricted utilization of germ-line VH3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B tymphocyte immunoglobulin heavy chain rearrangements
Eur. J. Immunol. 22 (1), 247-251 (1992)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                           1 GAGGTGCAGCTGGAGTCTGGGGGGGGTTGGTCAAGCCTGGAGGGTCCCTGAGACTC
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Ig CDR3 region; Ig heavy chain; Un element; rearranged gene;
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295 GTGACCCTGGGGGAT-----TGGGGCCAGGGAACCCTGGTCACCGTCTC 338
                                           42; Indels 12;
    Length 342;
    DB 9;
  Score 238.8; DB 9
Pred. No. 2.4e-53;
0; Mismatches 42,
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/cell_type="B_lymphocyte"
/tissue_type="liver"
/dev_stage="18 week old foetus"
|1. .290
/note="Vh_element"
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/isolate="Clone FL18-3"
/db xref="taxon:9606"
/chromosome="14"
Query Match
Best Local Similarity 84.6%;
Matches 296; Conservative
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Homo sapiens
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Raaphorst, F.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGGCGATCCCACA 180
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Board of Regents, The University of Texas System (US)
Location/Qualifiers
1. .351
CCFGTGCAGCCTCTG-----GATTCACCTTCAGTGACTACTACATGAGCTGGATCCGCC
                                                                                                                                                                                                                      AGGCTCCAGGGCAGGGGTGGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT
                                                                                                                                                                                                                                                                                        TGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCT
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295 ACGGGTTTTCCGGGGTTTGACTATTGGGGCCAAGGTACCCTGGTCACCGTCTC 347
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fmol type="unassispaed DNA"
db stref="texton:32630"
/db cref="synthetic Coding Sequence"
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                                                                                                /product="imminoglobulin heavy chain variable region"
/protein_id="AAC51069.1"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Human anti-adipocyte monoclonal antibodies and their use
Patent: WO 012/279-A. 155. 19-APR-2001;

Cambridge Antibody Technology (GB)

Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                   /gene="V3-23"
/note="Ig VH3 heavy chain"
/codon_start=1
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Sequence 155 from Patent WO0127279.
AX112674
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/translation="EVQLVESGGGLVQPGGSLRLSCSASGFTFSSYAMHWVRQAPGKG
LEYVSAISSNGGSTYYADSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCVKSRGP
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                  348 bp mRNA linear PRI 02-JUL-2002
Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
partial cds, clone:H249.
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TGGTACGCAGACTCCGTGAAGGCAGATTCACCATCTCCAGAGAGAACACCAACAACACA 240
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Catarrhini, Hominidae, Homo.
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/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="immunoglobulin heavy chain VHDJ region"
/protein_id="BAC01527.1"
/db_xref="G1:21669000"
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Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujta Health University;
Kutsukake-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
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llarity 81.7%; Pred. No. 2.2e-52;
Conservative 0; Mismatches 58;
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Location/Qualifiers
1. .348
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="H249"
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Unpublished
2 (bases 1 to 348)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                             Homo sapiens
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Unpublisher
(Unpublisher)
(Gasea 1 to 354)
(Gase, A. W. and Milner, E.C.B.
Direct Submission
(G-FSB-2000) Virginia Mason Research Institute, 1201 9th
Submitted (G-FSB-2000) Virginia Mason Research Institute,
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/cali type="healthy B + bmt T"
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                     AF231402 354 bp mRNA linear PRI 13-JUN-2000 Homo sapiens clone 4-4 immunoglobulin heavy chain variable region AF231402 GI:8489289
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Welaryota's Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 354)

Glas, A.w., van Montfort, B.H.N., Storek, J., Green, R.N.,

Drissen, R.P., Bechtold, V.J., Reilly, J.Z., Dawson, M.A. and

Milner, B.C.B.
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Best Local Similarity 82.8%; Pred. No. 1.3e-52;
Matches 298; Conservative 0; Mismatches 50; Indels 12; Gaps
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/note="V3-23"
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Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone="aims0017h"
/clone lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
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Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Immunology, Kutsukake-cho, Toycake, Aichi 470-1192, Japan (E-mil:kurosawaofujita-hu.ac.jp, Tel:81-562-93-9387) Please višt our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
                                                                  301 TTGACTACAGGGTCTCACTCCGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
295 AGTCGGGGTTTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC 344
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2 (bases 1 to 351)
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ALIGNMENTS

BP.

Screening antibody; 2-D electrophoresis; plural protein; protein spot; antibody library; proteomics; ds. Antibody screening method related DNA VH(DP-47). (NISC-) JAPAN SCI & TECHNOLOGY CORP. (NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY. 05-JUN-2001; 2001WO-JP004732. 24-NOV-2000; 2000JP-00358539. (first entry) WPI; 2002-471742/50. P-PSDB; AA021548 WO200242774-A1. Unidentified. 30-MAY-2002. 02-SEP-2002 Kaneko K;

Screening an antibody using 2-D electrophoresis on plural proteins in samples for separating individual protein spots to react with an antibody library useful in proteomics and other biological sciences. Disclosure; Fig 1; 78pp; Japanese.

The invention relates to a novel method for screening an antibody, comprising performing 2-D electrophoresis on plural proteins in a sample. Individual protein spots are separated by reacting them with an antibody library and then replicating the bound antibodies before reacting them with the spot proteins again. The method is useful for screening an antibody specific for a target protein, e.g. from a phage antibody library, which is useful in proteomics for studying various protein and complementary decayribonucleic acid (cDNA) expression libraries as well as gene functions, and in other biological and medical sciences. This

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polynucleotide is a DNA sequence relating to the antibody screening method of the invention
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protein"
/note= "CDS does not include start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
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                                                                                           69.8%; Score 247.2; DB 6; Length 348; larity 82.6%; Pred. No. 5.4e-59; Conservative 0; Mismatches 55; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2C6 clone.
                                                           Sequence 348 BP; 71 A; 84 C; 108 G; 73 T; 0 U; 12 Other;
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P-PSDB; AAE28870.
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The invention relates to a method of inhibiting tumour growth which involves administering, vascular endothelial growth factor receptor (VEGER) antagonists in combination with radiation, chemotherapeutic gaput, or epidermal growth factor receptor (EGER) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, heart lung, small intestine, colon, spleen, bone marrow, blood, thymus, uterus, testicles, cervix or liver) over expresses VEGER; it is also useful for inhibiting growth of colon tumour or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGER.

It is preferably useful for treating subjects with both solid tumours, progression of tumour growth includes prevention or inhibition of the progression of tumour including cancerous and non-cancerous tumours, where the progression of tumours includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is human KDR (VEGER-2) Fab antibody heavy chain DNA
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Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 348;
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                                                                                                                                                                                                             Example 9; Page 121-122; 151pp; English
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The invention relates to a method of inhibiting tumour growth comprising administering to a human a vascular endothelial growth factor receptor vyGFRP, antagonist and epidermal growth factor receptor (BGFR) antagonist. The method is useful for inhibiting tumour growth. The present sequence is used in the exemplification of the invention.
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Human heavy chain variable region
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94US-00326552.
95US-00476533.
96US-00706804.
97US-00779450.
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P-PSDB; ADD24417.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for
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Pred. No. 2e-57;
0; Mismatches 5
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Matches 290; Conservative
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P-PSDB; ABJ26763.
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           WO2003002144-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTGCGCAGCCTCCGGGTTCAGGTTCACTTCAATAACTACAAGGACTGGGTCCGC 120
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                                                                      Human clone D2C6 KDR-binding Fab variable heavy chain gene SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGGTGCAGCTGGTGTGTCTGGGGGCGCTTGGCAAAGCCTGGGGGTCCCTGAGACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          New human anti-KDR antibody, useful for preparing a composition for reducing tumor growth and inhibiting angiogenesis.
                                                                                              human; antibody; KDR; cytostatic; gene therapy; anti-KDR antibody; tumour; angiogenesis; gene; ds.
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Pred. No. 2e-57;
0; Mismatches 54; Indels
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                                                                                                                                                                                                                 codon given"
                                                                                                                                                                                                      "KDR-binding Fab"
                                                                                                                                                                                                                    'note= "No start/stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 23; 49pp; English
                                                                                                                                                                 Socation/Qualifiers
                                                                                                                                                                                                                                                                                                 04-MAR-2003; 2003WO-US006459
                                                                                                                                                                                                                                                                                                                          04-MAR-2002; 2002US-0361783P
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Best Local Similarity 82.9%;
Matches 290; Conservative
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The invention relates to a method of inhibiting tumour growth which involves administering, vascular endothelial growth factor receptor (VBGFR) antagonists in combination with radiation, chemotherapeutic agent, or epidermal growth factor receptor (BGFR) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, head and neck, overy, prostate, brain, pancreas, skin, bone marrow, blood, thymus, uterus, testicles, cervix or liver) over cyprosesses VBGFR. It is also useful for inhibiting growth of colon tumour or non-small cell lung carcinoma (NSCLC) and tumour overexpressing BGFR. It is preferably useful for treating subjects with both solid tumours, preferably useful for treating subjects with both solid tumours, reduction of tumour growth includes prevention or inhibition of the progression of tumour includes prevention or inhibition of the progression of tumours includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is human KDR (VBGFR-2) Fab antibody heavy chain DNA Human; tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC; breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene; VH; Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor /*tag= a /product= "Human KDR (VEGFR-2) Fab heavy chain (VH) protein" /note= "CDS does not include start and stop codon" Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D1H4 clone. Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other; Example 12; Page 124-125; 151pp; English. Location/Qualifiers 1. .348 04-MAR-2002; 2002WO-US006762 02-MAR-2001; 2001US-00798689 (IMCL-) IMCLONE SYSTEMS INC. AAD46292 standard; DNA; 348 (first entry) /partial GOLDSTEIN N I. WPI; 2002-691738/74. P-PSDB; AAB28870. WO200270008-A1 Homo sapiens. antagonists. 27-DEC-2002 12-SEP-2002 AAD46292; (ROCK/) (GOLD/) Key g à

New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGP) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors. The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VBGF) receptor and a second antigen-binding site specific for a second VBGF receptor. The bispecific antigen-binding proteins block activation of the VBGF receptor and are seful for reducing or inhibiting VBGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating 300 TCCTGCGCAGCCTCCGGGTTCAGGTTCACCTCAATAACTACTACATGGACTGGGTCCGC 120 114 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180 174 240 234 crerarcrecaargaacaeccreagaeccgaegacacacecrererarracrerecaaga 294 9 9 mitogenesis; CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATTAGTAGTAGTAGTAGTAGTACATA TACTACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 61 recrerecadecrere----earreacerreagracranacardaacresecee TGGTACGCAGACTCCGTGAAGGCAGATTCACCATCTCCAGAGAACGCCAACAACACA rescharecoreseggiccoreagactic Gaps 295 GICACAGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTC 344 TTGACTACAGGGTCTGACTCCTGGGGGCCAGGGAGTCCTGGTCACCGTCTC 350 9 Cytostatic; antibody; antigen binding site; VEGF receptor; m leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; human; gene; ds. Score 240; DB 6; Length 348; Pred. No. 5.5e-57; 0; Mismatches 55; Indels GAGGTGCAGCTGGTGGAGTCTGGGGGGCGCC VEGF binding related DNA SEQ ID No 79. Disclosure; Page 72; 98pp; English. 67.8%; 82.6%; 26-JUN-2002; 2002WO-US020332 26-JUN-2001; 2001US-0301299P ABT23327 standard; DNA; 348 (IMCL-) IMCLONE SYSTEMS INC (first entry) Best Local Similarity 82.6 Matches 289; Conservative WPI; 2003-201468/19. WO2003002144-A1. 01-MAY-2003 Homo sapiens 09-JAN-2003 235 115 175 241 301 61 181 Query Match Ñ Zhu RESULT 7

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                                                                                                                                                                                CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC
                                           1 GAGGTGCAGCTGCAGTCTGGCGGCCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                                                                                  TOCTGOGCAGOCTTCCGGGTTCACCTTCAATAACTACATGGACTGGGTCCGC
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  Length 348;
Score 240; DB 7; Length 34
Pred. No. 5.5e-57;
0; Mismatches 55; Indels
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94US-00326552.
95US-0076533.
95US-00779450.
97US-00967113.
99US-00401163.
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    67.8%;
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             Best Local Similarity 82.6
Matches 289; Conservative
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P-PSDB; ADD24417.
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                                                                                                                                                                                                                                                                                                                                                                                                                   tumour; vascular epidermal growth
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20-OCT-1994;
07-JUN-1995;
03-SEP-1996;
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10-NOV-1997;
22-SEP-1999;
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tumours and for in vivo or in vitro for investigative and diagnostic methods. This polynucleotide sequence represents a human DNA sequence relating to the bispecific antibodies that bind to the VEGF receptors

Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other;

the invention

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IMCLONE SYSTEMS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of inhibiting tumour growth comprising administering to a human a vascular endothelial growth factor receptor (WGSPR) antegonist and epidermal growth factor receptor (BGFR) antagonist. The method is useful for inhibiting tumour growth. The present sequence is used in the exemplification of the invention.
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                  Inhibiting tumor growth by administering to a human a vascular endothelial growth factor receptor (VEGFR) antagonist and epidermal growth factor receptor (EGFR) antagonist.
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                                                                                                                                                                                                                                                                                  tch 67.8%; Score 240; DB 9; sal Similarity 82.6%; Pred. No. 5.5e-57; 289; Conservative 0; Mismatches 55
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/product= "KDR-bindir.
/note= "No start/stop
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epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;
breast; VBGFR; heart; BGFR; therapy; invasiveness; heavy chain; gene; VH;
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/product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
protein"
                                                                               New human anti-KDR antibody, useful for preparing a composition for reducing tumor growth and inhibiting angiogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGGTGCAGCTGGTGGAGTCTGGGGGCTTGGCAAAGCCTGGGGGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.8%; Score 240; DB 9;
Best Local Similarity 82.6%; Pred. No. 5.5e-57;
Matches 289; Conservative 0; Mismatches 55
                                                                                                                                                                    Example 1; SEQ ID NO 27; 49pp; English
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1. .348
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WPI; 2003-779032/73.
P-PSDB; ADD80794.
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involves administering, vascular endothelial growth factor receptor (VEGER) antagonists in combination with radiation, chemotherapeutic agent to repidermal growth factor receptor (EGER) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, heard and neck, ovary, prostate, brain, pancreas, skin, bone marrow, blood, thymus, uterus, testicles, cervix or liver) over expresses vEGER: It is also useful for inhibiting growth of colon tumour or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR. It is preferably useful for treating subjects with both solid tumours, preferably useful for treating subjects with both solid tumours, or reduction of tumour growth includes prevention or inhibition of the progression of tumour including cancerous and non-cancerous tumours, where the progression of tumour includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is tumour CDE and in DNA.
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                                                                                                                                                                                                                                                                                                                                  Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of inhibiting tumour growth which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 238.4; DB 6; Length 348; Pred. No. 1.5e-56; O; Mismatches 56; Indels 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 12; Page 126; 151pp; English.
                                                                                                                 04-MAR-2002; 2002WO-US006762
                                                                                                                                                       02-MAR-2001; 2001US-00798689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 67.3%;
al Similarity 82.3%;
288; Conservative
                                                                                                                                                                                                  IMCLONE SYSTEMS INC.
                                                                                                                                                                                             (IMCL-) IMCLONE SYSTEM:
(ROCK/) ROCKWELL P.
(GOLD/) GOLDSTEIN N I.
                                                                                                                                                                                                                                                                              2002-691738/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            WPI; 2002-691738/
P-PSDB; AAE28873.
                                     WO200270008-A1
                                                                           12-SEP-2002,
                                                                                                                                                                                                                                                                                                                                                                                                    antagonists,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (WEGF) receptor and a second antigen-binding site specific for a second vEGF receptor. The bispecific antigen-binding proteins block activation of the WEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leuksemia cells. The antibodies are useful for tracting tumours and for in vivo or in vitro for investigative and diagnostic methods. This polynucleotide sequence represents a human DNA sequence relating to the bispecific antibodies that bind to the VEGF receptors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                         Cytostatic, antibody, antigen binding site, VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGCTCCAGGGCAGGGCTGCAGTGGGTCTCACTATTAGTAGTAGTGGTGATCCCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTGCCCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACTAGGACTGGGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 73-74; 98pp; English.
                                                                                                          82
                                                                                                          VEGF binding related DNA SEQ ID No
               BP
                                                                                                                                                                                                                                                                                                        26-JUN-2002; 2002WO-US020332.
                                                                                                                                                                                                                                                                                                                                       26-JUN-2001; 2001US-0301299P.
               ABT23329 standard; DNA; 348
                                                                                                                                                                                                                                                                                                                                                                      (IMCL-) IMCLONE SYSTEMS INC.
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-201468/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
288; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABJ26765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating tumors.
                                                                                                                                                                                                                                       WO2003002144-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention
                                                                                                                                                                                                            Homo sapiens.
                                                                             01-MAY-2003
                                                                                                                                                                                                                                                                        09-JAN-2003.
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                                              ABT23329
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                                                                                                                                                                                                                                                                                                                                                                                                       Zhu Z;
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ABT23329
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                                                                                       ADD80800 standard; DNA; 348
                                                                                                                                                                                                                                                   29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-779032/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ADD80801
                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003075840-A2.
                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                 241
                                                                                                                                                                                                                             ADD80800;
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                                                                                                                                                                                 RESULT 13
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TCTGCGCAGCCTCCGGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of inhibiting tumour growth comprising administering to a human a vascular endothelial growth factor receptor (VEGFR) antagonist and epidermal growth factor receptor receptor antagonist. The method is useful for inhibiting tumour growth. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGCTGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting tumor growth by administering to a human a vascular endothelial growth factor receptor (VEGFR) antagonist and epidermal growth factor receptor (BGFR) antagonist.
                                                                                                                                                                                                     tumour; vascular endothelial growth factor receptor; VBGFR; epidermal growth factor receptor; BGFR; cancer; human; ds; gene.
                                   TIGACIACAGGGICTGACTCCIGGGGCCAGGGAGTCCIGGTCACCGTCTC 350
                                                   295 GFCACAGAFGCTITIFGATAFCFGGGGCCAAGGGACAATGGTCACCGFCFC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 238.4; DB 9; Length 3
Pred. No. 1.5e-56;
0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 U; 0 Other;
                                                                                                                                                                                 Human heavy chain variable region DNA #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 12; SEQ ID NO 30; 90pp; English.
                                                                                                                                                                                                                                                                                                                            10-FEB-1994; 94US-00196041.

20-0CT-1994; 94US-00326552.

07-JUN-1995; 95US-00476533.

03-SEP-1996; 96US-00706804.

07-JAN-1997; 97US-00779450.

10-NOV-1997; 97US-00967113.

22-SEP-1999; 99US-00401163.

02-MAR-2001; 2001US-00798689.
                                                                                                               ADD24423 standard; DNA; 348 BP
                                                                                                                                                                                                                                                                                                        04-MAR-2002; 2002US-00091300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 82.3%;
Matches 288; Conservative (
                                                                                                                                                           15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rockwell P, Goldstein NI;
                                                                                                                                                                                                                                                                                                                                                                                                                                         GOLDSTEIN N 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-801265/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ADD24424.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ROCKWELL
                                                                                                                                                                                                                                                            US2003108545-A1.
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                    12-JUN-2003
                                   301
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                                                                                                                                                                                                                                                                                                                                                                                                                               (ROCK/)
(GOLD/)
                                                                                         RESULT 12
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The invention relates to a novel isolated human antibody or its fragment binds selectively to KDR. An antibody of the invention has cytostatic activity, and may have a use in gene therapy. The antibody is anti-KDR antibody. The antibody is useful for preparing a composition for reducing tumour growth and inhibiting anislogenesis. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Η,
175 TACTACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAAGGACTCA 234
                                                                                                                                                                                                                                                                                      CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGCCTGTCTATTACTGTGCGAGC 300
                                                                                                                                                                                                                                                                                                                             235 CIGTATCTGCAAATGAACAGCTGAGAGCCGAGACACGCCTGTGTATTACTGTGCGAGA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human clone D2H2 KDR-binding Fab variable heavy chain gene SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAGTGCAGCTGGTGCAGTCTGGGGGGGCCTGGTCAAGCCTGGGGGTCCCTGAGACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human anti-KDR antibody, useful for preparing a composition for reducing tumor growth and inhibiting angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; antibody; KDR; cytostatic; gene therapy; anti-KDR antibody; tumour; angiogenesis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                             301 TIGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 Greacagardentricanarergedeceaagegacaardereacerere 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "KDR-binding Fab"
/note= "No start/stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.3%; Score 238.4; DB 9
Best Local Similarity 82.3%; Pred. No. 1.5e-56;
Matches 288; Conservative 0; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 30; 49pp; English.
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                                                                                                                    recrerecade creation ----- carreactreactare caracacarda a creation con contra c
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62 CCTGTGCAGCCTCTG-----GATTCACCTTCAGTGACTACTACATGAGCTGGATCCGCC 115

CCTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC 121

62

122

2 AGGIGCAGCIGGIGGAGICIGGGGGGGGGGCTGGGGGGGTCCCTGAGACTCT

61

Gaps

. 9

Indels

Length 348;

DB 4; 26;

Score 237.4; DB 4 Pred. No. 2.9e-56; 0; Mismatches 56

tch 67.1%; al Similarity 82.2%; 287; Conservative

Query Match Best Local S Matches

Sequence 348 BP; 79 A; 91 C; 108 G; 70 T; 0 U; 0 Other;

heart disease

116 addoriccadddaadddachddadhddaracarrachadadhacrachadaracha 175

AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGGTGATCCCACAT 181

236 IGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACGACGCCGTGTATTACTGTGCGAGAG 295

296 Accidadenderrocarcicriosocicadescacicridercacidaring 344

302 TGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC

350

242 TGTTTCTTCAAATGAACAGCCTGAGGACTGAGGACACGGCTGTTTACTGTGCGAGCT 301

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26-10 scFv antibody light chain; complementarity determining region 3; CDR3; binding protein production; catalytic protein production; ds; ligand structure determination; antibody isolation; dig3 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                     Obtaining bacterium having nucleic acid encoding binding protein that binds target ligand, or a nucleic acid encoding catalytic protein that
                                                                                                                                                                                                                                                                                                                                                                  Ö
                                                                                                                                                                                                           partial
product= "Dig3 heavy chain"
/note= "No start or stop codon is given"
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                                                                                     Dig3 antibody heavy chain coding sequence.
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                  AAL43586 standard; DNA; 351 BP
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P-PSDB; AAO15187.
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                                                                                                                                                     Unidentified
                                                                05-SEP-2002
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                                          AAL43586;
RESULT 15
                                                                                                                                                                             Key
            AAL43586
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19803401-AAS03535 represent anti-adipocyte monoclonal antibody heavy and light chain coding sequences of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself.

Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an adipocyte sin a cell or tissue sample. The antibodies can be used as an adipocyte seans of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra- abdominal fat associated with

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catalyzes reaction involving target substrate by display-less library screening.
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Example 4; Page 97; 98pp; English

The invention comprises a method of obtaining a bacterium containing a nucleic acid encoding a binding protein capable of binding a target ligand, or a nucleic acid encoding a catalytic protein that catalyses a reaction involving a target substrate. The method of the invention allows the isolation of a cell expressing a nucleic acid encoding a binding protein capable of binding a target ligand, and consequently the isolation of the nucleic acid encoding a binding isolation of the nucleic acid. The binding protein produced by the method of the invention is useful in determining the structure of a target ligand. The method of the invention is useful for the de novo isolation of antibodies from large repertoire libraries and for monitoring production during protein manufacturing. The method can also be used for monitoring production of a particular byproduct of a biological reaction. The present DNA sequence encodes the dig3 scFv antibody heavy chain which is used in an example of the invention

Sequence 351 BP; 77 A; 85 C; 109 G; 80 T; 0 U; 0 Other;

174 235 CIGIALCHGCAAATGAACAGCCTGAGAGCGGAGACACGGCCGTGTATTACTGTGCAAGA 294 recredecacerreacerreacerreacerreacerreariasariacareaceregerrese 120 TOSTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAGGCCCAACACACA 240 175 TACTACGCAGACTCTGTGAAGGCCGATTCACCATCTCCAGGGACAAGGAACTCA 234 CIGITICITICAAATGAACAGCCIGAGAGCIGAGACACGCCIGICIATTACIGIGCGAGC 300 61 TCCTGTGCGCCTCTG-----GATTCACCTTCAGTGACTACTACTAGAGCTGGATCGC 114 121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGATCCCACA 180 9 1 GAGGTGCAGCTGGTGGAGTCTGGGGGGAGGCTTGGTCAAGCCTGCAGGGTCCCTGAGACTC 60 1 CAGGIGCAGCIGGIGGAGICIGGGGGCGCTIGGCAAAGCCIGGGGGGCCCTGAGACTC 9; Gaps 301 TTG---ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350 DB 6; Length 351; Indels 66.8%; Score 236.6; DB 6; 83.6%; Pred. No. 4.9e-56; ive 0; Mismatches 49; Query Match
Best Local Similarity 83.6
Matches 295; Conservative 181 241 61 음 g ठे g ò g ò ઠે ò à a

Search completed: June 19, 2004, 08:21:28 Job time : 283 secs

11, Appli 1, Appli 1, Appli 55, Appli 54, Appl 51, Appl 17, Appl 17, Appl 139, Appl 139, Appl 14, Appl 14, Appl 138, Appl 14, Appl 14, Appl 138, Appl

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RESULT 1

US-08-652-816A-21

US-08-652-816A-21

Sequence 21, Application US/08652816A

Patent No. 5872215

GENERAL INFORMATION:
APPLICANT: OSPOURT, JK

APPLICANT: Allen, DJ

APPLICANT: MCCAfferty, JG

TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: Methods.

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADRESS:
ADRESSES: Marshall: O'Toole, Gerstein, Murray & Borun STREET: Glions
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPITY: United States of America
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: DatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION UNDER: US/08/652,816A
FILING DATE: 23-MAY-1996
FILING DATE: 02-D62-1991
PRIOR APPLICATION DATE:
APPLICATION UNDER: GB 9125579.8
FILING DATE: 24-MAR-1992
FILING DATE: 24-MAR-1992
FILING DATE: 24-MAR-1992
FILING DATE: 34-MAR-1992
US-08-791-391A-1
US-07-916-615-1
US-07-918-344A-9
US-08-477-553A-55
US-08-477-553A-51
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PULING DATE: 23-SEP-1992

RELOR PAPLICATION DATE:

APPLICATION DATE:

PULING DATE: 07-DEC-1995

PILING DATE: 07-DEC-1995

PRIOR APPLICATION DATE:

APPLICATION NUMBER: GB 9610824.6

FILING DATE: 23-MAY-1996

PRIOR APPLICATION NUMBER: BCT/GB92/02240

PILING DATE: 02-DEC-1995

PRIOR APPLICATION NUMBER: PCT/GB92/02240

PILING DATE: 02-DEC-1995

RILING DATE: 02-DEC-1997

APPLICATION NUMBER: PCT/GB92/02240

PILING DATE: 02-DEC-1997

APPLICATION NUMBER: PCT/GB92/02240

PILING DATE: 01-UNN-1994

APPLICATION NUMBER: DCT/GB92/02240

PILING DATE: 01-UNN-1994
      176.2
175.6
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      21, Appl
22, Appl
35, Appl
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-652-816A-22
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US-08-428-197-47
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US-08-958-201-1
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UG-08-652-816A-22

UG-08-652-816A-22

Sequence 22, Application US/08652816A

Sequence 22, Application US/08652816A

GENERAL INFORMATION:
APPLICANT: OSDOUTN, JK

APPLICANT: ALIEN, DJ

APPLICANT: McCafferty, JG

TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Illinois
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: D'. Wersion #1.25 (BPO)
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
RIUNG DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
FILING DATE: 02-DEC-1991
FILING DATE: 02-DEC-1991
                                                                                                                                                                                                                                                            Length 354;
                                                                                                                                                                                                                                                                                          57; Indels
                                                                                                                                                                                                                                                         63.2%; Score 223.8; DB 2;
80.8%; Pred. No. 2e-60;
tive 0; Mismatches 57;
Best Local Similarity 80.8 Matches 290; Conservative
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US-08-652-816A-21
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175 TACTACGAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 CTGTTTCTTCAAATGAACAGCCTGAGGTGAGGACACGGCTGTCTATTACTGTGCGAG-
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Pred. No. 3e-60;
0; Mismatches 58; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRICRATION NUMBER: GB 9206312.6
PRICRATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRICRATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
FILING DATE: 07-DEC-1995
PRICRATION NUMBER: GB 9610824.6
FILING DATE: 07-DEC-1995
PRICRATION NUMBER: GB 9610824.6
FILING DATE: 07-DEC-1995
PRICRATION NUMBER: PCT/GB92/02240
PRICRATION NUMBER: PCT/GB92/02240
PRICRATION NUMBER: DCT/GB92/02240
PRICRATION NUMBER: DCT/GB92/02240
PRICRATION NUMBER: DCT/GB92/0240
PRICRATION NUMBER: US 08/244,597
FILING DATE: 01-JUN 1994
ATTORNEY-AGENT INPORMATION:
NAME: DAVIG W. CLOUGH
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPERENCE/DOCKET NUMBER: 36,107
REPERENCE/DOCKET NUMBER: 28111/33308
TELESCOMMUNICATION INFORMATION:
FORMATION: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 24, Application US/08652816A; Patent No. 5872215; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312-474-6300 INFORMATION FOR SEQ ID NO: 22:
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80.6%;
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LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.6
Matches 290, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-08-652-816A-22
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US-08-652-816A-24
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ADDRESSEE:

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8: Spensley Horn Jubas & Lubitz
1880 Century Park Bast - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 Sequence 35, Application US/08428197 Patent No. 5891438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Howells, Stacy L. REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: FD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.13
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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IMMEDIATE SOURCE:
CLONE: SPA3-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
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                                                                                                                                                                                                                               US-08-428-197-35
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                                                                                                                                                                                                            RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAAGGCCCAAACAACAA 240
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.: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 05/08/652,816A
FILING DATE: 23-MAY-1996
FRIDNG APPLICATION NUMBER: 08 9125579.4
APPLICATION NUMBER: 08 9125579.4
FRIDNG APPLICATION NUMBER: 08 9125579.4
FRIDNG APPLICATION NUMBER: 08 9125579.8
FRIDNG APPLICATION NUMBER: 08 9206318.9
FRIDNG APPLICATION NUMBER: 08 9206318.9
FRIDNG APPLICATION NUMBER: 08 9206318.9
FRIDNG APPLICATION NUMBER: 08 9206312.6
FRIDNG APPLICATION NUMBER: 08 9206312.6
FRIDNG APPLICATION NUMBER: 08 9206372.6
FRIDNG APPLICATION NUMBER: 08 9206372.6
FRIDNG APPLICATION NUMBER: 08 952004.9
FRIDNG APPLICATION NUMBER: 08 9610824.6
FRIDNG APPLICATION NUMBER: 08 9610824.6
FRIDNG APPLICATION NUMBER: 07-DEC-1995
FRIDNG APPLICATION NUMBER: 07-DEC-1995
FRIDNG APPLICATION NUMBER: 07-DEC-1995
FRIDNG APPLICATION NUMBER: 02-DEC-1997
APPLICATION NUMBER: 02-DEC-1997
FRIDNG APPLICATION NUMBER: 02-DEC-1997
FRIDNG APPLICATION NUMBER: 02-DEC-1997
APPLICATION NUMBER: 03-DEC-1997
FRIDNG APPLICATION NUMBER: 03-DEC-1997
APPLICATION NUMBER: 03-DEC-1997
APPLICATION NUMBER: 03-DEC-1997
FRIDNG APPLICATION NUMBER: 03-DEC-1997
AP
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                                                                                    STATE: Illinois
COUNTRY: United States of America
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 79.4%;
Matches 278; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 348 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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               STREET: Chicago
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US-08-652-816A-24
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Best Local
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GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
235 CTGTATCTTCAAATGAAGAGTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 GCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACATGGACTGGGTCCGCCAGGCT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 CTGCTCGAGGAGTCTGGGGGGAGGCTTGGTACAGCCTGGGGTGCCCCTGAGACTCTCTTGT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 CAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTCCTGC
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                                                                                   301 TIGACIACAGGGICTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
                                                                                                                                                                            295 AGGCGGTATGCGTTGGATTATTGGGCCCAAGGTACCCTGGTCACCGTGTC 344
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127 CCAGGGCAGGGGTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACACATGGTAC 186
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
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PRICR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: FD.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Spal-29
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INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION:
US-08-428-197-41
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SILVERMAN, GREGG J.
FUNTION: METHOD FOR STIMULATING PRODUCTION OF
FUNTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
FENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
FENTION: THEREOF
                                                  181 GCCGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGAACGCCAAGAACTCACTGTAT 240
                                                                                                                           247 CTTCAAATGAACAGCCTGAGAGCTGAGACGCGCTGTCTATTACTGTGCGAGCTTGAC- 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...ureSSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
XIP: 9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: PCT/US93/10555
29-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34 942
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                             CT-US93-10555-35
Sequence 35, Application PC/TUS9310555
GENERAL INFORMATION: APPLICANT: SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD TITLE OF INVENTION: VAR TITLE OF INVENTION: THE NUMBER OF SEQUENCES: 51 CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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MOLECULE TYPE:
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Sequence 41, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: WARHABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
187 GCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTGTTT 246
                                                                       181 GCCGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTAT 240
                                                                                                                                                  247 CTTCAAATGAACAGCCTGAGAGCTGACACGCCTGTCTATTACTGTGCGAGCTTGAC- 305
                                                                                                                                                                                                                          241 Checaameaacaeccheaeaecceaaeacaceecherenarrachereceaeaeaneca 300
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60.5%; Score 214.2; DB 2; Length 345;
Best Local Similarity 79.6%; Pred. No. 1.9e-57;
Matches 281; Conservative 0; Mismatches 63; Indels 9.
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121

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GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: WETHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THERBOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AddoriccadedaAddedecredaAgredercreagrafraGreccaGresfaAraccaCar 175
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                                                                                                                                                                                                                                                                                                                                                                                               122 AGGCTCCAGGGCAGGGGGTGGAGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT 181
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                                                                                                                                                                                                                               62 CCTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AGGIGCAGCIGGAGICTGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCT
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 TGACTACAGGGTCTGACTCCTGGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
    6
    63; Indels
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COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Spensley Horn Jubas & Lubitz STREET: 1880 Century Park East - Suite 500 CITY: Los Angeles STATE: California COUNTRY: USA
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INPORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: FD-2630
TELECOMMUNICATION INPORMATION:
"""TREPOND: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47, Application US/08428197
Patent No. 5891438
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IMMEDIATE SOURCE:
CLONE: VH26C
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TELEPAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 47
SEQUENCE CHARACTERISTICS:
LENGTH: 294 base pairs
TYPE: nucleic acid
            Conservative
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            281;
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            Matches
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Sequence 41, Application:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
SILVERMAN, GREGG J.
TITLE OF INVENTION: WARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACINATION WITH A B-CELL SUPERANTIGEN AND COMJUGATES
TITLE OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
A
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                                                                                                                              62 CCTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC 121
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    2 AGGTGAAACTGCTCCAGTCTGGGGGAGCTTGGTACAGCCTGGGGGGGTCCCTGAGACTCT
                                                                                                                                                                                                                                                                                                   122 AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGATCCCACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 TGACTACAGGGTCTGACTCCTGGGCCCAGGGAGTCCTGGTCACCGTCTCCTCA
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MEDTING TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PACHOLIN PC-DOS/MS-DOS
SOFTWARE: PACHOLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILLING DATE: 29-OCT-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 214.2; DB 5;
Pred. No. 1.9e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Spensley Horn Jubas & Lubitz
1880 Century Park Bast - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFRENCE/DOCKET NUMBER: FD-2.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 1..345
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Best Local Similarity
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CLONE: SpA1-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 18
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PCT-US93-10555-41
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                                                                                                                                                                                             Gaps
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                                                                                                                          Length 294;
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Parent No. 597319
GENERAL INFORMATION:
APPLICANT: Pritchard, Kevin
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Revin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCES 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall O'Toole Gerstein Murray & Bo
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                      Score 213.6; DB 5;
Pred. No. 2.8e-57;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-0CT-1996
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                              Query Match
Best Local Similarity 84.9%;
Matches 253; Conservative
                             1..294
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TOPOLOGY: JIME
IMMEDIATE SOURCE:
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                             LOCATION:
PCT-US93-10555-47
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; LOCATION:
US-08-958-201-1
NAME/KEY:
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TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND COMJUGATES
TITLE OF INVENTION: THEREOF
CORRESPONDENCE: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAGGCCAACAACACAA 240
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                                                                                                                                                                                                                                             Gabs
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                                                                                                                                                                   Score 213.6; DB 2; Length 294;
Pred. No. 2.8e-57;
0; Mismatches 39; Indels 6;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, Stacy L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 36,945
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEPHONE: CHARACTERISTICS:
FOWLTH: 294 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park Bast - Suite 500
CIIY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 47, Application PC/TUS9310555 GENERAL INFORMATION:
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Best Local Similarity 84.9%;
Matches 253; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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                                     ; NAME/KEY:
; LOCATION:
US-08-428-197-47
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       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 CAGACTCCAGACAAGAGGCTGGAGGTGGCAACCATTAATAGTAATGGTGGTCTCACC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 ----GCTTGACTACAGGGTCTGACTCCTGGGGCCCAGGGAGTCCTGGTCACCGTCTCCTCA
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                                             1 GAGGTGCAGTTGGAGTCTGGGGGCTTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                                                                                                                                                                                                                                         121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA
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                                                                                              1 caggrecaacregregaaaccegeeeeecrregracaeccregeeeerccreaaaacre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Otterness, Ivan G.
APPLICANT: Otterness, Ivan G.
APPLICANT: Deter S.
APPLICANT: Dens, James T.
APPLICANT: Downs, James T.
APPLICANT: Downs, James T.
APPLICANT: Downs, James T.
TITLE OF INVENTION: Biological Media
TITLE OF INVENTION: Biological Media
FILE REFERENCE: PC9946-A
CURRENT APPLICATION NUMBER: U$/09/184,658
CURRENT PILING DATE: 1998-11-02
RABLIER PILING DATE: 1998-11-13
NUMBER: PELONG DATE: 1997-11-13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
12; Gaps
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  74; Indels
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  0; Mismatches
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NAME/KEY: V region
LOCATION: (1)..(348)
CTHER INFORMATION: Mature 5109 VH region.
US-09-184-658-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-184-658-10; Sequence 10, Application US/09184658; Patent No. 6030792; BENERAL INFORMATION:
     274; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                   121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                                                                                 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 240
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                                                                                                                    9
                                                                                                                  GAGGTGCAGCTGGTGGAGTCTGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTC
                                                                         1 GAGGTGCAGCTGGTGGAGTCTGGGGGCCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pope, Anthony R
APPLICANT: Prichard, Kevin
APPLICANT: Prichard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Williams
SPARES: Williams
CITY: Chicago
STATE: 111inois
                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/958,201
FILING DATE:
PAIOR APPLICATION DATA:
APPLICATION NAMER: US 60/028,897
FILING DATE: 21-OCT-1996
INFORMATION PRE SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FRIGH: 354 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 354;
  Pred. No. 9.5e-57;
0; Mismatches 65; Indels
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Pred. No. 5.3e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08958201
Patent No. 5977319
GENERAL INFORMATION:
APPLICANT: Pope, Anthony R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.5%;
76.1%;
  Best Local Similarity 78.6%;
Matches 283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity
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IMMEDIATE SOURCE:
CLONE: 1C
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HOCATION:
US-08-958-201-3
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US-08-958-201-3
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; Sequence 185455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 GTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTCTCCTGCGCAGCCTCCGGGTTCAG
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OTHER INFORMATION: Concerted to the properties of Fig. 11/14. No OTHER INFORMATION: Conceptions 24-362 of Fig. 11/14. No OTHER INFORMATION: 1-23 and 363-378 represent PCR primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.7%; Score 190; DB 2; Length 339;
83.3%; Pred. No. 6.9e-50;
ive 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 GAGAGCGAAGACACGCTGTGTATTACTGTGCAAG 270
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                                                                                                                                                                                                                                                                                                                    #1.25
          COMPUTER: USA
COMPUTER: READMEBE FORM:
MEDDIUM TYPE: FLORPY disk
COMPUTER: READMEBE FORM:
MEDDIUM TYPE: FLORPY disk
COMPUTER: READMEBE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/477,553A
FLING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,034
FLING DATE: 13-NOW-1999
ATTORNEY/AGENT INPORMATION:
NAME: Meth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
REFERENCE (703) 836-6620
TELLEPHONE: (70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
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Best Local Similarity 83.3<sup>3</sup>
Matches 230; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pfizer Inc.
APPLICANT: Saltarelli, Mary J.
APPLICANT: Johnson Kimberly S.
APPLICANT: Johnson Kimberly S.
APPLICANT: Otherness, Ivan G.
TITLE OF INVENTION: Assays for Measurement of Type II Collagen Fragments in Urine FILE REFERENCE: PC10189GPR - CIP of PC9946A
CURRENT APPLICATION NUMBER: US/09/504,262D
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3:1
SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGCTCCAGGGGCAGGGGCTGGAGTGTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAGGCCAACAACACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 TTTATGCAGACAGTGTGAAGGGCCGATTCACCATTCCAGAGACAATGCCAAAAACAC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
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                                                                                     CTGTTTCTTCAAATGAACAGCCTGAAAGGTGAAGGACAGGCTGTCTATTACTGTGCGAGC 300
                                                                                                                                                                                 235 CTGTATCTGCAAATGAACAGGCTGAAGTCTGGGGACTCAGGCATGTATTACTGTGTAAGA 294
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175 ITTTATGCAGACAGTGTGAAGGCCGATTCACCATTTCCAGAGACAATGCCAAAAACACC 234
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                                                                                                                                                                                                                                                                                                                                   295 GGATATAAGTAATTAAGGCTCGCTGGGGCCCAAGGGGGCGCTGGTCATCTCTGCA 348
                                                                                                                                                                                                                                                                                      301 TIGACTACAGGGICTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCTCA 354
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; Sequence 52, Application US/08477553A
; Patent No. 591930
; GENERAL INFORMATION:
APPLICANT: HIGHES-JONES, Nevin C
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
; ADDRESSER: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09504262D
Patent No. 6642007
GENERAL INFORMATION:
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Best Local Similarity 74.3
Matches 263; Conservative
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CONGANISM: Mus musculus
US-09-504-262D-10
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Best Local Similarity 74.5%; Pred. No. 3.4e-49;
Matches 266; Conservative 0; Mismatches 82; Indels 9
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH17
FEATURE:
                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: anti-Rh(D) antibody clone SH17 US-09-240-274-184
                       FILE REFERENCE: 05596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
BARLIER APPLICATION NUMBER: 60/081,380
BARLIER FILING DATE: 1998-04-10
BARLIER PILING DATE: 1998-04-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Perentin Ver: 2.0
SOFTWARE: Perentin Ver: 2.0
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Job time : 64 secs
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ORGANISM: Homo sapiens
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17, Appl 18, Appl 24519, A 13, Appl 175, App

Sequence Sequence

Sequence 24519, A Sequence 113, Appl Sequence 17, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 11, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 34, Appli Sequence 21, Appli Sequence 22, Appli Sequence 25, Appli Sequence 55, Appli

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APPLICANT: Rockwell, Patricia
APPLICANT: Rockwell, Neil I.
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
GURRENT 11245/46211
GURRENT APPLICATION NUMBER: US/10/091,300
GURRENT PILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 IGGIACGCAGACICCGTGAAGGGCAGAITCACCAICICCAGAGAGAAGGCCCAACAACACA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82.9%; Pred. No. 1.8e-66;
Matches 290; Conservative 0; Mismatches 54; Indels
                                                                                                                                                                           08-09-974-449-1

3 US-01-147-849-4

6 US-10-1147-849-4

6 US-10-113-551-13

7 US-10-408-901-21

3 US-09-948-939-14

3 US-09-948-939-14

5 US-10-10-10-129-34

6 US-09-995-529-7

2 US-09-995-529-7

2 US-09-995-529-7

3 US-09-996-529-7

6 US-09-996-529-7

7 US-10-408-901-25

6 US-10-318-366-51

6 US-10-29-346-55-39

6 US-10-029-386-25-39

6 US-10-251-215-19

8 US-10-257-8644-55

7 US-10-29-386-25-39

6 US-10-257-8644-55

7 US-10-29-386-25-39
US-10-038-591-31
US-10-120-377-74
US-10-120-377-74
US-10-251-215-18
US-10-029-386-24519
US-10-408-901-13
US-10-432-409A-175
US-10-338-366-1
US-10-251-215-21
US-10-251-215-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/10091300 Publication No. US20030108545A1 GENERAL INFORMATION:
     TYPE: DNA
CRGANISM: Human
US-10-091-300-23
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193.8
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                                                     211.4
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Sequence 15, Appl
Sequence 11, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 21, Appli
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Sequence 27, Appl
Sequence 30, Appl
Sequence 25, Appl
Sequence 18, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 29, Appl
                                                                                                                   June 19, 2004, 08:52:24; Search time 285 Seconds (without alignments) 5690.195 Million cell updates/sec
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/ cgn2_6/prodata/2/pubpna/USO7_PUBCOMB.seq:*
/ cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
/ cgn2_6/prodata/2/pubpna/USO6_PUBCOMB.seq:*
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/ cgn2_6/prodata/2/pubpna/USO9_NEW_PUB.seq:*
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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G US-10-091-300-27

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US-10-466-836-25

US-10-269-711-18

US-10-269-711-18

US-10-251-215-17

US-09-864-761-3123

US-10-251-215-17

US-10-324-493-15

US-10-324-493-15

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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published
                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 354
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Match
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Maximum DB
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No.
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Gaps

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DB 15; Length 348;

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Query Match 67.3%;
Best Local Similarity 82.3%;
Matches 288; Conservative
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Best Local Similarity 82.4%
Matches 294; Conservative
                                                                                         TYPE: DNA
CRGANISM: Human
US-10-091-300-30
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ORGANISM: HUMAN
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APPLICANT: Rockwell, Patricia
APPLICANT: Rockwell, Neil I.
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular FILLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
FILE REFERENCE: 11245/46211
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8:0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30, Application US/10091300
Publication No. US2030108545A1
CENERAL INPORMATION:
APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist FILE PERENCE: 11245/46211
CURRENT APPLICANTON NUMBER: US/10/091,300
CURRENT PILING DATE: 2002-03-04
175 TACTACGCAGACTCAGTGAAGGCCGATTCACCATCTCCAGAGACACAACGCCAAGAACTCA 234
                                                                    241 CTGTTTCTTCAAATGAACAGCCTGAGGCTGAGGACACGGCTGTCTATTACTGTGCGAGG 300
                                                                                            61 TCCTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
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                                                                                                                                                                                                                                                                                         US-10-691-300-27; Application US/10091300; Sequence 27, Application US/10091300; Publication No. US20030108545A1; PNERRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Human
US-10-091-300-27
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US-10-091-300-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Best Local 8
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Sequence 25, Application US/10466936
FUBLICATION NO. US20040110922A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION CHIMBER BIO-APPLICATIONS LTD.
TITLE OF INVENTION CHIMBER US/10/466,836
CURRENT APPLICATION NUMBER: US/10/466,836
CURRENT APPLICATION NUMBER: L141023
FRICE RIPLE APPLICATION NUMBER: L141023
FRICE FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 26
SEQ ID NOS: 26
SEQ ID NOS: 26
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                                                                                                                                                                                                                                                   67.3%; Score 238.4; DB 15; Length 348; 82.3%; Pred. No. 1.9e-65; tive 0; Mismatches 56; Indels 6;
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NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 30
LENGTH: 348
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APPLICANT:

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241 CTGTTTCTTCAAATGAACAGCCTGAGGACACGGCTGTCTTTTACTGTGCGA-- 298
235 CTGTATCTGCAAATGAACAGCCTGAGAGCGGAGGACACGGCGGTGTTTACTGTGCAAGA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 AGCTCCAGGCAAGGGCTGGGAGTGGCTGGCAGTTTAATGGTATGAAGAAGTAATAAAT 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGGTGCAGCTGGTGGAGTCGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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                                                                                                                                                                                   299 -GCTTGACTACAGGTCTGACTCCTGGGCCAGGGGTCCTGGTCACGGTCTCCTCA 354
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                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/10269711
Sequence 18, Application US/10269711
GENERAL INFORMATION:
APPLICANT: Aboott Laboratories
APPLICANT: Belly, Edward B.
APPLICANT: Reller, James
APPLICANT: Weiler, James
APPLICANT: Weiler, James
TITLE OF INVENTION: BRYTHRPPOIETIN RECEPTOR BINDING
TITLE OF INVENTION: ANTIBODIES
FILE REFREENCE: 6989 US.01
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT PILIG DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 349
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; ORGANISM: Homo sapiens
US-10-269-711-18
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US-10-269-711-38
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US-10-269-711-18
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Sequence 38, Application US/10269711; Publication No. US20040071694A1; GENERAL INFORMATION: APPLICANT: Abbort Laboratories; APPLICANT: DeVries, Peter J.

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APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Katherine S.
APPLICANT: Kretz-Rommel, Anke
APPLICANT: Frederickson, Shana
TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINERED
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 1087-36
CURRENT APPLICATION NUMBER: US 40/323,537
FRIOR APPLICATION NUMBER: US 60/323,537
FRIOR FILING DATE: 2001-09-20
FRIOR FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 17
LENGTH: 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 TCTATGCAGACTCCGTGAAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 CCTGCGCAGCCTCCGGGTTCAGGTTCAATAACTACTACATGGACTGGGTCCGCC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 AGSCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 TGTTTCTPCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCT 301
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                       63.2%; Score 223.8; DB 12; Length 79.3%; Pred. No. 8.1e-61; ive 0; Mismatches 67; Indels
            APPLICANT: Ostrow, Dave
APPLICANT: Weiler, James
APPLICANT: Weiler, James
APPLICANT: Green, Larry
APPLICANT: Green, Larry
APPLICANT: Green, Larry
TITLE OF INVENTION: ERYTHRODIES
FILE REPRENCE: 6989.US.OI
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 38
LUMB NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/10251215; Publication No. US20030219839A1; GENERAL INFORMATION:
Reilly, Edward B.
Ostrow, Dave
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 280; Conservative
                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-10-269-711-38
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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; ORGANISM: human
US-10-251-215-17
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Sequence 29, Application US/10038591
| Publication No US20040086503A1
| Publication No US20040086503A1
| GENERAL INPORMATION:
| APPLICANT: Cohen, Bruce D. |
| APPLICANT: Miller, Penelope B. |
| APPLICANT: Moyer, James D. |
| APPLICANT: Moyer, James D. |
| APPLICANT: Corvalan, Jose R. |
| APPLICANT: Corvalan, James D. |
| APPLICANT: Corvalan, ANTIBODIES TO INSULIN-LIKE GROWTH PACTOR I RECEPTOR |
| TITLE OF INVENTION NATIBODIES TO INSULIN-LIKE GROWTH PACTOR I RECEPTOR |
| TITLE OF INVENTION NATIBODIES TO INSULIN-LIKE GROWTH PACTOR I RECEPTOR |
| FILE REPRENCE: 2002-01-04
| PRIOR FILING DATE: 2002-01-04
| PRIOR FILING DATE: 2001-01-05
| NUMBER: OF SEQ ID NOS: 60
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 29
| LEMOTH: 296
| THOSE FILE OF INVENTION OF 296
| THOSE FILE OF INVENTION OF 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGFATTAGTAGTAGTGGTGATCCCACA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAAACGCCAACAACACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 FACTACGCAGACTCAGTGAAGGGCCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGGTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGGGGG 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 311;
                                                                                                                                                                                                            TYPE: DNA
OKCANIEM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.51
OTHER INFORMATION: EST HUMAN HIT: AM403220.1, EVALUE 0.00e+00
OTHER INFORMATION: M HIT: L29155.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: P01764, EVALUE 3.00e-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.9%; Score 222.6; DB 9; Length 3
Best Local Similarity 86.6%; Pred. No. 1.9e-60;
Matches 259; Conservative 0; Mismatches 34; Indels
       PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31233
LENGTH: 311
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Matches 258; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-864-761-31233
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Patent No. US20020048763A1

GENERAL INCORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL POR TILE DF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION UNMERR: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR PRING DATE: 2000-05-23

PRIOR PRING DATE: 2000-02-04
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                                                                                                                                                                                                                                                                              61 TCCTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                               61 TCCTGTGCAGCCTCTG-----GATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGC 114
                                                                                                                                                                                                                                                                                                                                                                                                             121 CAGGCTCCAGGGCAGGGGCTGGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 240
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                                                                                                                                                                               GAGGIGCAGCTGGIGGAGTCTGGGGGGGCCTGGGCTCAAGCCTCGGGGGTCCCTGAGACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAAACTC 60
Query Match 62.9%; Score 222.6; DB 16; Length 294;
Best Local Similarity 86.6%; Pred. No. 1.9e-60;
Matches 259; Conservative 0; Mismatches 34; Indels 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/20/312
PRIOR APPLICATION NUMBER: US 60/20/456
PRIOR APPLICATION NUMBER: US 60/20/456
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
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US-09-864-761-31233
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Sequence 15, Application US/10324493

Publication No. US2003012412141

GENERAL INFORMATION:

APPLICANT: Pluenneke, John

TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF

FILE REPERSENCE: 3005-C

CURRENT PILING DATE: 2002-12-19

PRIOR APPLICATION NUMBER: US/09/847,816

PRIOR PILING DATE: 2001-05-01

PRIOR PILING DATE: 2001-05-26

PRIOR PILING DATE: 2001-05-26

PRIOR PILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 09/665,343

PRIOR PILING DATE: 2000-09-19

PRIOR PILING DATE: 2001-02-15

PRIOR FILING DATE: 2001-02-15

WUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIN VERSION 3.0

SEQ ID NOS: 26

SEQ ID NO 12-15

SEQ ID NOS: 26

SEQ ID NOS: 26

SEQ ID NOS: 26
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PRICE APPLICATION WINDER: US/10324493

PUBLICANT: PLUEDMARION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF FILE REFRENCE: 3005-C

FILE REFRENCE: 3005-C

CURRENT FILING DATE: 2002-12-19

PRICE APPLICATION NUMBER: US/09/847,816

PRICE APPLICATION NUMBER: US/09/847,816

PRICE APPLICATION NUMBER: 09/5-01

PRICE APPLICATION NUMBER: 09/5-01

PRICE APPLICATION NUMBER: 09/5-03

PRICE FILING DATE: 2000-05-26

PRICE FILING DATE: 2000-05-26

PRICE FILING DATE: 2000-05-19

PRICE FILING DATE: 2000-05-19

PRICE FILING DATE: 2000-05-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 CCTGTTCAGCGTCTG-----GATTCACCTTCAGTAGATATGGCATGCATGGCCCCCC
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2.7e-59;
ches 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 61.9%;
Best Local Similarity 78.5%;
Matches 277; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)..(348)
US-10-324-493-15
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APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Katherine S.
APPLICANT: Breat-Cason, Shana
TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 1087-36
CURRENT APPLICATION NUMBER: US 60/323,537
PRIOR APPLICATION NUMBER: US 60/323,537
PRIOR APPLICATION NUMBER: US 60/323,54
PRIOR FILING DATE: 2001-09-20
PRIOR FILING DATE: 2001-09-20
PRIOR FILING DATE: 2001-09-20
PRIOR PLING DATE: 2001-09-20
PRIOR PLING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 20
LENGTH: 294
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                                                                                                   122 AGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT 181
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                                                                   CCTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC
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Best Local Similarity 86.0%; Pred. No. 1.9e-59;
Matches 257; Conservative 0; Mismatches 36; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/10251215 Publication No. US20030219839A1 GENERAL INFORMATION:
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RESULT 11 US-10-324-493-15

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Squence 1, Application US/10460595

Squence 1, Application US/10460595

Publication No. US2040067532A1

GENERAL INFORMATION:
APPLICANT: But, il.
APPLICANT: Hua, Shaobing B

TITLE OF INVENTION: HIGH THROUGHPUT GENERATION AND AFFINITY MATURATION OF HUMANIZED
TITLE REFERENCE: 25636-730

CURRENT FILING DATE: 2003-06-11
PRIOR PRING PATE: 2002-06-11

PRIOR PRING DATE: 2002-08-12

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 296
                                                                                                                                                                                                                               121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGATCCCACA 180
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                                                                                                                                                               61 TCCTGTGCGAGCCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
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                                  GAGGTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC
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. OTHER PROPAGATION: Consensus human germline VH sequence (DP47)
US-10-460-595-1
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ORGANISM: Artificial Sequence
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Matches 255; Conservative
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US-10-460-595-1
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Fublication No US20030124121A1
GENERAL INPORMATION:
GENERAL INPORMATION:
TILLE OF INVENTION:
TILLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/324, 493
CURRENT FILING DATE: 2002-12-19
FRICA PELICATION NUMBER: US/10/324, 493
FRICA FILING DATE: 2001-05-01
FRICA FILING DATE: 2001-05-01
FRICA FILING DATE: 2000-05-26
FRICA FILING DATE: 2000-05-26
FRICA FILING DATE: 2000-09-19
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                                                                                                                                                                                                                                                                                                 61.7%; Score 218.4; DB 15; Length 345; 80.2%; Pred. No. 4.2e-59; tive 0; Mismatches 61; Indels 9;
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PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.25
Matches 284; Conservative
                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-10-324-493-11
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US-10-324-493-23
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                                                                          SEQ ID NO 11
LENGTH: 345
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LENGTH: 351
                                                                                                                                                                            FEATURE
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US-10-038-591-31

| Sequence 31, Application US/10038591
| Sequence 31, Application US/10038591
| Sequence 31, Application US/20040086503A1
| Publication No. US20040086503A1
| APPLICANT: Cohen, Bruce D. | APPLICANT: Miller, Penelope E. | APPLICANT: Miller, Penelope E. | APPLICANT: Corvalan, Jose R. | APPLICANT: Corvalan, Jose R. | APPLICANT: Corvalan, Jose R. | APPLICANT: Gallo, Michael | ITLLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR | FILE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR | TILLE OF INVENTION NUMBER: US/10/038,591 | CURRENT APLICATION NUMBER: 60/259,927 | PRIOR FILING DATE: 2002-01-04 | PRIOR FILING DATE: 2001-01-05 | NUMBER OF SEQ ID NOS: 60 | SOOTHARE: Patentin Ver. 2.1 | SEQ ID NO 31 | LENGTH: 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCCAGAGAGAACACCAACAACAACA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-10-038-591-31
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